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(54) **ANGIOGENESIS-ASSOCIATED PROTEINS, AND NUCLEIC ACIDS ENCODING THE SAME**
ANGIOGENESE-ASSOZIIERTE PROTEINE UND DAFÜR KODIERENDE NUKLEINSÄURE
PROTEINES ASSOCIEES A L'ANGIOGENESE ET ACIDES NUCLEIQUES CODANT CES
PROTEINES

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Functions as a Transcriptional Repressor"
MOLECULAR AND CELLULAR BIOLOGY, vol. 18,
no. 7, July 1998 (1998-07), pages 4235-4244,
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Description

[0001] Cities have roads and alleys, plants have xylem and phloem, and people have arteries, veins and lymphatics. Without these byways, the vertebrate animal cells would starve or drown in their metabolic refuse. Not only do blood vessels deliver food and oxygen and carry away metabolic wastes, but they also transport signaling substances that apprise cells of situations remote to them but to which they need to respond. Hormonal messages are a common signal.

[0002] All blood vessels are ensheathed by a basal lamina and a delicate monolayer of remarkably plastic endothelial cells lining the luminal walls. Depending on location and function, smooth muscle and connective tissue may also be present

[0003] Not only do healthy cells depend on the blood resources transported by the circulatory system, but so, too, unwanted cells: tumorigenic and malignant cells. These cells colonize and proliferate if they are able to divert blood resources to themselves. Angiogenesis, the type of blood vessel formation where new vessels emerge from the proliferation of preexisting vessels (Risau, 1995; Risau and Flamme, 1995), is exploited not only by usual processes, such as in wound healing or myocardial infarction repair, but also by tumors themselves and in cancers, diabetic retinopathy, macular degeneration, psoriasis, and rheumatoid arthritis. Regardless of the process, whether pathological or usual physiological, endothelial cells mediate angiogenesis in a multi-step fashion: (1) endothelia receive an extracellular cue, (2) the signaled cells breach the basal lamina sheath, abetted by proteases they secrete, (3) the cells then migrate to the signal and proliferate, and finally, (4) the cells form a tube, a morphogenic event (Alberts *et al.*, 1994). The complexity of this process indicates complex changes in cellular physiology and morphology, gene expression, and signaling. Angiogenic accomplices that are cues include basic fibroblast growth factors (bFGF), angiopoietins (such as ANG1) and various forms of vascular endothelial growth factor (VEGF).

[0004] The molecular events and the order in which they occur and the pathways that are required for this process are of fundamental importance to understand angiogenesis. *In vitro* models are useful for identifying alterations in gene expression that occur during angiogenesis. A particularly fruitful model systems involves the suspension in a three-dimensional type I collagen gel and various stimuli, such as phorbol myristate acetate (PMA), basic fibroblast growth factor (bFGF), and VEGF. The combination of the stimuli and the collagen gel results in the formation of a three-dimensional tubular network of endothelial cells with interconnecting luminal structures. In this model, endothelial differentiation into tubelike structures is completely blocked by inhibitors of new mRNA or protein synthesis. Furthermore, the cells progress through differentiation in a coordinated and synchronized manner, thus optimizing the profile of gene expression (Kahn *et al.*, 2000; Yang *et al.*, 1999).

[0005] Tumor cells exploit angiogenesis to facilitate tumor growth. Controlling angiogenesis, by controlling the activity or expression of genes and proteins associated with angiogenesis, provides a way to prevent tumor growth, or even destroy tumors. Database EMBL (Online) 3 July 1998, Okabe, S. *et al.* Acc. No. AB011665; and Okabe, S. *et al.* Molecular and Cellular Biology, Vol. 18, No. 7, July 1998, pages 4235-4244, describes murine BAZF and its function as a transcriptional repressor.

[0006] The present invention provides an isolated polypeptide comprising an amino acid sequence having at least 90% sequence identity to the sequence of SEQ ID NO: 4, wherein expression of the polypeptide is upregulated during angiogenesis.

[0007] The present invention also provides an isolated polynucleotide comprising a nucleotide sequence having at least 80% sequence identity to the sequence of SEQ ID NO: 3, or a complement of said polynucleotide, wherein expression of the polynucleotide is upregulated during angiogenesis.

[0008] The invention is based in part upon the discovery of novel nucleic acid sequences encoding novel polypeptides. Nucleic acids encoding the polypeptides disclosed in the invention, and derivatives and fragments thereof, will hereinafter be collectively designated as "AAP" nucleic acid or polypeptide sequences. AAP, or angiogenesis associated polypeptides (AAP) comprise human ortholog of mouse BAZF (hBAZF).

[0009] In a first aspect, the present invention is an isolated polypeptide having at least 90% sequence identity to the sequence SEQ ID NO : 4. polynucleotides encoding the same, and antibodies that specifically bind the same.

[0010] In a second aspect, the present invention is an isolated polynucleotide having at least 80% sequence identity to the sequence SEQ ID NO: 3, or a complement thereof.

[0011] In a third aspect, the present invention is a transgenic non-human animal, having a disrupted AAP gene or a transgenic non-human animal expressing an exogenous polynucleotide having at least 80% sequence identity to the sequence SEQ ID NO : 3, or a complement of said polynucleotide.

[0012] In an eighth aspect, the present invention is a method of measuring a AAP transcriptional and translational up-regulation or down-regulation activity of a compound.

[0013] In a ninth aspect, the invention is a method of screening a tissue sample for tumorigenic potential.

[0014] In a tenth aspect, the invention is a method of determining the clinical stage of tumor which compares the expression of at least one AAP in a sample with expression of said at least one gene in control samples.

[0015] Although methods and materials similar or equivalent to those described herein can be used in the practice or

testing of the present invention, suitable methods and materials are described below. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

[0016] A model of angiogenesis-the suspension of endothelial cells in type I collagen gels with various stimuli-was used to identify a molecular fingerprint or transcriptional profile of endothelial differentiation into tubelike structures, using amplification and an imaging approach called GeneCalling (Shimkets *et al.*, 1999). This method was previously shown to provide a comprehensive sampling of cDNA populations in conjunction with the sensitive detection of quantitative differences in mRNA abundance for both known and novel genes. Many differentially expressed cDNA fragments were found. The identification and differential expression of these genes was confirmed by a second independent method employing real-time quantitative polymerase chain reaction (PCR). Although some of the identified cDNA fragments were genes known to play some role in angiogenesis, many other differentially expressed genes were unexpected. The inventors have identified the unexpected genes and polypeptides that are expressed in response to this model of angiogenesis, collectively referred to as angiogenesis associated polypeptides (AAP). AAP is human ortholog of mouse BAZF (hBAZF).

[0017] Unless defined otherwise, all technical and scientific terms have the same meaning as is commonly understood by one of skill in the art to which this invention belongs. The definitions below are presented for clarity.

[0018] The recommendations of (Demerec *et al.*, 1966) where these are relevant to genetics are adapted herein. To distinguish between genes (and related nucleic acids) and the proteins that they encode, the abbreviations for genes are indicated by *italicized* (or underlined) text while abbreviations for the proteins start with a capital letter and are not italicized. Thus, *AAP* or AAP refers to the nucleotide sequence that encodes AAP.

[0019] "Isolated," when referred to a molecule, refers to a molecule that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that interfere with diagnostic or therapeutic use.

[0020] "Container" is used broadly to mean any receptacle for holding material or reagent. Containers may be fabricated of glass, plastic, ceramic, metal, or any other material that can hold reagents. Acceptable materials will not react adversely with the contents.

1. Nucleic acid-related definitions

(a) control sequences

[0021] Control sequences are DNA sequences that enable the expression of an operably-linked coding sequence in a particular host organism. Prokaryotic control sequences include promoters, operator sequences, and ribosome binding sites. Eukaryotic cells utilize promoters, polyadenylation signals, and enhancers.

(b) operably-linked

[0022] Nucleic acid is operably-linked when it is placed into a functional relationship with another nucleic acid sequence. For example, a promoter or enhancer is operably-linked to a coding sequence if it affects the transcription of the sequence, or a ribosome-binding site is operably-linked to a coding sequence if positioned to facilitate translation. Generally, "operably-linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by conventional recombinant DNA methods.

(c) isolated nucleic acids

[0023] An isolated nucleic acid molecule is purified from the setting in which it is found in nature and is separated from at least one contaminant nucleic acid molecule. Isolated *AAP* molecules are distinguished from the specific *AAP* molecule, as it exists in cells. However, an isolated *AAP* molecule includes *AAP* molecules contained in cells that ordinarily express an *AAP* where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

2. Protein-related definitions

(a) purified polypeptide

[0024] When the molecule is a purified polypeptide, the polypeptide will be purified (1) to obtain at least 15 residues of N-terminal or internal amino acid sequence using a sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or silver stain. Isolated polypeptides include those expressed heterologously in genetically-engineered cells or expressed *in vitro*, since at least one component of an *AAP* natural

environment will not be present. Ordinarily, isolated polypeptides are prepared by at least one purification step.

(b) *active polypeptide*

[0025] An active AAP or AAP fragment retains a biological and/or an immunological activity of the native or naturally-occurring AAP. Immunological activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native AAP; biological activity refers to a function, either inhibitory or stimulatory, caused by a native AAP that excludes immunological activity. A biological activity of AAP includes, for example, modulating angiogenesis.

(c) *Abs*

[0026] Antibody may be single anti-AAP monoclonal Abs (including agonist, antagonist, and neutralizing Abs), anti-AAP antibody compositions with polypepitopic specificity, single chain anti-AAP Abs, and fragments of anti-AAP Abs. A "monoclonal antibody" refers to an antibody obtained from a population of substantially homogeneous Abs, *i.e.*, the individual Abs comprising the population are identical except for naturally-occurring mutations that may be present in minor amounts

(d) *epitope tags*

[0027] An epitope tagged polypeptide refers to a chimeric polypeptide fused to a "tag polypeptide". Such tags provide epitopes against which Abs can be made or are available, but do not interfere with polypeptide activity. To reduce anti-tag antibody reactivity with endogenous epitopes, the tag polypeptide is preferably unique. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues, preferably between 8 and 20 amino acid residues). Examples of epitope tag sequences include HA from *Influenza A* virus and FLAG.

[0028] The novel AAP of the invention include the nucleic acid whose sequence is provided in Table 3. The invention also includes a mutant or variant AAP, any of whose bases may be changed from the corresponding base shown in Table 3, while still showing at least 80% identity with the polynucleotide provided in Table 3 and encoding a protein that maintains the activities and physiological functions of the AAP fragment. The invention further includes nucleic acids whose sequences are complementary to those just described. The invention additionally includes nucleic acids or complements thereto, whose structures include chemical modifications. Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as anti-sense binding nucleic acids in therapeutic applications in a subject. In the mutant or variant nucleic acids, and their complements, up to 20% or more of the bases may be so changed.

[0029] The novel AAP of the invention include the protein fragment whose sequence is provided in Table 4. The invention also includes an AAP mutant or variant protein, any of whose residues may be changed from the corresponding residue shown in Table 4, while still showing at least 90% identity with the polypeptide of Table 4 while still encoding a protein that maintains its native activities and physiological functions. The invention further encompasses Abs and antibody fragments, such as F_{ab} or (F_{ab})₂, that bind immunospecifically to any of the AAP of the invention.

[0030] The AAP nucleic acid is shown in Table 3, and the corresponding polypeptides is shown in Table 4, respectively. Start and stop codons in the polynucleotide sequences are indicated in boldface and with underlining. SEQ ID NO:3 lacks a stop codon. For any lacking polynucleotide sequence, one of skill in the art may retrieve the full length sequence by, for example, probing cDNA or genomic libraries with probes designed according to the sequences of the instant invention.

Table 3 hBAZF nucleotide sequence (SEQ ID NO:3)

5	caagggagcg aggggtgctg agagggcaga atgaacaaga agaattagga gggaggctgc	60
	gtgtgccggg gctaggggct ggaagtcctg gctctagttg cacctcggaa ggaaaaggca	120
	aacagaggag ggaaggcgtc ttaggactgc ctggatccag agcactttcc tcggcctcta	180
	caggcctgtg tcgctatggg ttcccccgcc gccccggagg gagcgctggg ctacgtccgc	240
10	gagttcactc gccactcctc cgacgtgctg ggcaacctca acgagctgcg cctgcgcggg	300
	atcctcactg acgtcacgct gctggttggc gggcaacccc tcagagcaca caaggcagtt	360
	ctcatcgctt gcagtggctt cttctattca attttccggg gccgtgcggg agtcgggggtg	420
	gacgtgctct ctctgccggg ggggtcccgaa gcgagaggct tcgccccctct attggacttc	480
15	atgtacactt cgcgcctgcg cctctctcca gccactgcac cagcagtcct agcggccgcc	540
	acctatttgc agatggagca cgtggtccag gcatgccacc gcttcatcca ggccagctat	600
	gaactcttgg gcatctccct gcgccccctg gaagcagaac cccaacacc cccaacggcc	660
	cctccaccag gtagtcccag gcgctccgaa ggacaccag acccacctac tgaatctcga	720
20	agctgcagtc aaggcccccc cagtccagcc agccctgacc ccaaggcctg caactggaaa	780
	aagtacaagt acatcgtgct aaactctcag gcctcccaag cagggagcct ggtcggggag	840
	agaagtcttg gtcaaccttg cccccaagcc aggtcctcca gtggagacga ggctccagc	900
	agcagcagca gcagcagcag cagcagcagt gaagaaggac ccattcctgg tcccagagc	960
25	aggctctctc caactgctgc cactgtgcag ttcaaagtgt gggctccagc cagtaccccc	1020
	tacctctca catcccaggc tcaagacacc tctggatcac cctctgaacg ggctcgtcca	1080
	ctaccgggga gtgaattttt cagctgccag aactgtgagg ctgtggcagg gtgctcatcg	1140
	gggctggact ccttggttcc tggggacgaa gacaaacct ataagtgtca gctgtgccgg	1200
30	tcttcgttcc gctacaaggg caaccttgcc agtcaccgta cagtgcacac aggggaaaag	1260
	ccttaccact gctcaatctg cggagccgtt tttaaccggc cagcaaacct gaaaacgcac	1320
	agccgcatcc attcgggaga gaagccgtat aagtgtgaga cgtgcggctc gcgctttgta	1380

35	caggtaggga gccagcctcc aagtggcttc caaggcaaac ctgcaagagg tgggggtgggc	1440
	caaaagggag ggttctgttc ctcccagagg caggacttga agtctcctcc ctcccagggtg	1500
40	gcacatctgc gggcgacgt gctgatccac accggggaga agccctacc ttgccctacc	1560
	tgcggaaccc gcttcgcca cctgcagacc ctcaagagcc acgttcgcat ccacaccgga	1620
	gagaagcctt accactgcga cccctgtggc ctgcatttcc ggcacaagag tcaactgcgg	1680
45	ctgcatctgc gccagaaaca cggagctgct accaacacca aagtgcacta ccacattctc	1740
	ggggggccc	1749

Table 4 hBAZF polypeptide sequence (SEQ ID NO:4)

Met	Gly	Ser	Pro	Ala	Ala	Pro	Glu	Gly	Ala	Leu	Gly	Tyr	Val	Arg	Glu	
1				5					10					15		
Phe	Thr	Arg	His	Ser	Ser	Asp	Val	Leu	Gly	Asn	Leu	Asn	Glu	Leu	Arg	
			20					25					30			
Leu	Arg	Gly	Ile	Leu	Thr	Asp	Val	Thr	Leu	Leu	Val	Gly	Gly	Gln	Pro	
		35					40					45				
Leu	Arg	Ala	His	Lys	Ala	Val	Leu	Ile	Ala	Cys	Ser	Gly	Phe	Phe	Tyr	
	50					55					60					
Ser	Ile	Phe	Arg	Gly	Arg	Ala	Gly	Val	Gly	Val	Asp	Val	Leu	Ser	Leu	
65					70					75					80	
Pro	Gly	Gly	Pro	Glu	Ala	Arg	Gly	Phe	Ala	Pro	Leu	Leu	Asp	Phe	Met	
				85					90					95		
Tyr	Thr	Ser	Arg	Leu	Arg	Leu	Ser	Pro	Ala	Thr	Ala	Pro	Ala	Val	Leu	
			100					105					110			
Ala	Ala	Ala	Thr	Tyr	Leu	Gln	Met	Glu	His	Val	Val	Gln	Ala	Cys	His	
		115					120					125				
Arg	Phe	Ile	Gln	Ala	Ser	Tyr	Glu	Pro	Leu	Gly	Ile	Ser	Leu	Arg	Pro	
	130					135					140					
Leu	Glu	Ala	Glu	Pro	Pro	Thr	Pro	Pro	Thr	Ala	Pro	Pro	Pro	Gly	Ser	
145					150					155					160	
Pro	Arg	Arg	Ser	Glu	Gly	His	Pro	Asp	Pro	Pro	Thr	Glu	Ser	Arg	Ser	
				165					170					175		
Cys	Ser	Gln	Gly	Pro	Pro	Ser	Pro	Ala	Ser	Pro	Asp	Pro	Lys	Ala	Cys	
			180					185					190			
Asn	Trp	Lys	Lys	Tyr	Lys	Tyr	Ile	Val	Leu	Asn	Ser	Gln	Ala	Ser	Gln	
		195					200					205				
Ala	Gly	Ser	Leu	Val	Gly	Glu	Arg	Ser	Ser	Gly	Gln	Pro	Cys	Pro	Gln	
	210					215					220					

5

Ala Arg Leu Pro Ser Gly Asp Glu Ala Ser Ser Ser Ser Ser Ser Ser
225 230 235 240

10

Ser Ser Ser Ser Ser Glu Glu Gly Pro Ile Pro Gly Pro Gln Ser Arg
245 250 255

Leu Ser Pro Thr Ala Ala Thr Val Gln Phe Lys Cys Gly Ala Pro Ala
260 265 270

Ser Thr Pro Tyr Leu Leu Thr Ser Gln Ala Gln Asp Thr Ser Gly Ser
275 280 285

15

Pro Ser Glu Arg Ala Arg Pro Leu Pro Gly Ser Glu Phe Phe Ser Cys
290 295 300

Gln Asn Cys Glu Ala Val Ala Gly Cys Ser Ser Gly Leu Asp Ser Leu
305 310 315 320

20

Val Pro Gly Asp Glu Asp Lys Pro Tyr Lys Cys Gln Leu Cys Arg Ser
325 330 335

Ser Phe Arg Tyr Lys Gly Asn Leu Ala Ser His Arg Thr Val His Thr
340 345 350

25

Gly Glu Lys Pro Tyr His Cys Ser Ile Cys Gly Ala Arg Phe Asn Arg
355 360 365

Pro Ala Asn Leu Lys Thr His Ser Arg Ile His Ser Gly Glu Lys Pro
370 375 380

30

Tyr Lys Cys Glu Thr Cys Gly Ser Arg Phe Val Gln Val Arg Ser Gln
385 390 395 400

Pro Pro Ser Gly Phe Gln Gly Lys Pro Ala Arg Gly Gly Val Gly Gln
405 410 415

35

Lys Gly Gly Phe Cys Ser Ser Gln Arg Gln Asp Leu Lys Ser Pro Pro
420 425 430

Ser Gln Val Ala His Leu Arg Ala His Val Leu Ile His Thr Gly Glu
435 440 445

40

Lys Pro Tyr Pro Cys Pro Thr Cys Gly Thr Arg Phe Arg His Leu Gln
450 455 460

Thr Leu Lys Ser His Val Arg Ile His Thr Gly Glu Lys Pro Tyr His
465 470 475 480

45

Cys Asp Pro Cys Gly Leu His Phe Arg His Lys Ser Gln Leu Arg Leu
485 490 495

50

His Leu Arg Gln Lys His Gly Ala Ala Thr Asn Thr Lys Val His Tyr
500 505 510

His Ile Leu Gly Gly Pro
515

55

[0031] The invention also includes polypeptides having 90, 91, 92, 93, 94, 95, 96, 97, 98 and 99%, sequence identity to SEQ ID NOS: 4, as well as nucleotides encoding any of these polypeptides, and compliments of any of these nucle-

otides. In an alternative embodiment, polypeptides and/or nucleotides (and compliments thereof) identical to any one of, or more than one of, SEQ ID NOS: 3 or 4 are excluded. In yet another embodiment, polypeptides and/or nucleotides (and compliments thereof) having 81-100% identical, including 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98 and 99%, sequence identity to SEQ ID NOS: 3-4 are excluded.

[0032] The nucleic acids and proteins of the invention are potentially useful in promoting wound healing, for example after organ transplantation, or in the treatment of myocardial infarction, but also in treating tumors, and in cancers, diabetic retinopathy, macular degeneration, psoriasis, and rheumatoid arthritis. For example, a cDNA encoding AAP may be useful in gene therapy, and AAP proteins may be useful when administered to a subject in need thereof. The novel nucleic acid encoding AAP, and the AAP proteins of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of Abs that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

Human ortholog of mouse BAZF (hBAZF)

[0033] hBAZF (SEQ ID NO:4) is the human ortholog of mouse BAZF (GenBank AB011665; SEQ ID NO:20), BAZF is a Bcl-6 (LAZ3) homolog, a transcription repressor that controls germinal center formation and the T cell-dependent immune response. Expression of Bcl-6 negatively correlates with cellular proliferation: Bcl-6 suppresses growth associated with impaired mitotic S phase progression and apoptosis (Albagli *et al.*, 1999).

[0034] BAZF contains a BTB/POZ domain and five repeats of the Kruppel-like zinc finger motifs, instead of 6 in Bcl-6 (Okabe *et al.*, 1998). Expression of BAZF mRNA is relegated to heart and lung, unlike Bcl-6 mRNA, but is induced in activated lymphocytes as an immediate-early gene, like Bcl-6 (Okabe *et al.*, 1998).

[0035] The hBAZF sequence was derived by using tblastn (protein query -translated database) (Altschul *et al.*, 1997), with the mouse protein sequence (GenBank O88282; SEQ ID NO:21) that has homology to GenBank AC015918 (SEQ ID NO:22), a clone of *Homo sapiens* chromosome 17. Human BAZF contains five Kruppel-like zinc finger motif repeats and a BTB/POZ domain.

[0036] The peptide sequence, "RSQ...PQV" that is present in the human sequence, might represent an alternative spliced form of the gene. Alignment with mouse BAZF, and alignment with mouse and human Bcl-6 demonstrates that the four proteins are almost identical in this region, but only human BAZF has this inserted sequence.

[0037] hBAZF is upregulated in HUVE cells grown embedded in collagen gels but not as a monolayer grown on collagen. When HUVE cells are suspended in collagen, they do not proliferate. Analogous to the role of mBAZF plays a role in regulating cell proliferation (Okabe *et al.*, 1998), hBAZF plays a role in cell proliferation in HUVE suspended in collagen. Because of its high expression during vessel morphogenesis, hBAZF represents an excellent molecular marker, as well as an attractive target for various therapies to inhibit angiogenesis.

AAP polynucleotides

[0038] One aspect of the invention pertains to isolated nucleic acid molecules that encode AAP or biologically-active portions thereof. Also included in the invention are nucleic acid fragments sufficient for use as hybridization probes to identify AAP-encoding nucleic acids (*e.g.*, AAP mRNAs) and fragments for use as polymerase chain reaction (PCR) primers for the amplification and/or mutation of AAP molecules. A "nucleic acid molecule" includes DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs. The nucleic acid molecule may be single-stranded or double-stranded, but preferably comprises double-stranded DNA.

1. probes

[0039] Probes are nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or many (*e.g.*, 6,000 nt) depending on the specific use. Probes are used to detect identical, similar, or complementary nucleic acid sequences. Longer length probes can be obtained from a natural or recombinant source, are highly specific, and much slower to hybridize than shorter-length oligomer probes. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies. Probes are substantially purified oligonucleotides that will hybridize under stringent conditions to at least optimally 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 consecutive sense strand nucleotide sequence of SEQ ID NO: 3 or an anti-sense strand nucleotide sequence of these sequences; or of a naturally occurring mutant of these sequences.

[0040] The full- or partial length native sequence AAP may be used to "pull out" similar (homologous) sequences (Ausubel *et al.*, 1987; Sambrook, 1989), such as: (1) full-length or fragments of AAP cDNA from a cDNA library from any species (*e.g.* human, murine, feline, canine, bacterial, viral, retroviral, yeast), (2) from cells or tissues, (3) variants

within a species, and (4) homologues and variants from other species. To find related sequences that may encode related genes, the probe may be designed to encode unique sequences or degenerate sequences. Sequences may also be genomic sequences including promoters, enhancer elements and introns of native sequence *AAP*.

[0041] For example, an *AAP* coding region in another species may be isolated using such probes. A probe of about 40 bases is designed, based on an *AAP*, and made. To detect hybridizations, probes are labeled using, for example, radionuclides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin-biotin systems. Labeled probes are used to detect nucleic acids having a complementary sequence to that of an *AAP* in libraries of cDNA, genomic DNA or mRNA of a desired species.

[0042] Such probes can be used as a part of a diagnostic test kit for identifying cells or tissues which mis-express an *AAP*, such as by measuring a level of an *AAP* in a sample of cells from a subject *e.g.*, detecting *AAP* mRNA levels or determining whether a genomic *AAP* has been mutated or deleted.

2. isolated nucleic acid

[0043] An isolated nucleic acid molecule is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Preferably, an isolated nucleic acid is free of sequences that naturally flank the nucleic acid (*i.e.*, sequences located at the 5'- and 3'-termini of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, isolated *AAP* molecules can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell/tissue from which the nucleic acid is derived (*e.g.*, brain, heart, liver, spleen, *etc.*). Moreover, an isolated nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

[0044] A nucleic acid molecule of the invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO: 3, or a complement of this aforementioned nucleotide sequence, can be isolated using standard molecular biology techniques and the provided sequence information. Using all or a portion of the nucleic acid sequence of SEQ ID NO: 3, as a hybridization probe, *AAP* molecules can be isolated using standard hybridization and cloning techniques (Ausubel *et al.*, 1987; Sambrook, 1989).

[0045] PCR amplification techniques can be used to amplify *AAP* using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers. Such nucleic acids can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to *AAP* sequences can be prepared by standard synthetic techniques, *e.g.*, an automated DNA synthesizer.

3. oligonucleotide

[0046] An oligonucleotide comprises a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction or other application. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment of the invention, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of SEQ ID NO: 3, or a complement thereof. Oligonucleotides may be chemically synthesized and may also be used as probes.

4. complementary nucleic acid sequences; binding.

[0047] In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in SEQ ID NO: 3, or a portion of this nucleotide sequence (*e.g.*, a fragment that can be used as a probe or primer or a fragment encoding a biologically-active portion of an *AAP*). A nucleic acid molecule that is complementary to the nucleotide sequence shown in SEQ ID NO: 3, is one that is sufficiently complementary to the nucleotide sequence shown in SEQ ID NO: 3, that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in SEQ ID NO: 3, thereby forming a stable duplex.

[0048] "Complementary" refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term "binding" means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, van der Waals, hydrophobic interactions, and the like. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical

intermediates.

[0049] Nucleic acid fragments are at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full-length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice.

5. *derivatives, and analogs*

[0050] Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differ from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type. Homologs are nucleic acid sequences or amino acid sequences of a particular gene that are derived from different species.

[0051] Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, or 95% identity (with a preferred identity of 80-95%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions (Ausubel *et al.*, 1987).

6. *homology*

[0052] A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of AAP. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, different genes can encode isoforms. In the invention, homologous nucleotide sequences include nucleotide sequences encoding for an AAP of species other than humans, including, but not limited to: vertebrates, and thus can include, *e.g.*, frog, mouse, rat, rabbit, dog, cat, cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the exact nucleotide sequence encoding human AAP. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in SEQ ID NO: 4, as well as a polypeptide possessing AAP biological activity. Various biological activities of the AAP are described below.

7. *open reading frames*

[0053] The open reading frame (ORF) of an AAP gene encodes an AAP. An ORF is a nucleotide sequence that has a start codon (ATG) and terminates with one of the three "stop" codons (TAA, TAG, or TGA). In this invention, however, an ORF may be any part of a coding sequence that may or may not comprise a start codon and a stop codon. To achieve a unique sequence, preferable AAP ORFs encode at least 50 amino acids.

AAP polypeptides

1. *mature*

[0054] An AAP can encode a mature AAP. A "mature" form of a polypeptide or protein disclosed in the present invention is the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, by way of nonlimiting example, the full-length gene product, encoded by the corresponding gene. Alternatively, it may be defined as the polypeptide, precursor or proprotein encoded by an open reading frame described herein. The product - "mature" form arises, again by way of nonlimiting example, as a result of one or more naturally occurring processing steps as they may take place within the cell, or host cell, in which the gene product arises. Examples of such processing steps leading to a "mature" form of a polypeptide or protein include the cleavage of the N-terminal methionine residue encoded by the initiation codon of an open reading frame, or the proteolytic cleavage of a signal peptide or leader sequence. Thus a mature form arising from a precursor polypeptide or protein that has

residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining after removal of the N-terminal methionine. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues from residue M+1 to residue N remaining. Further as used herein, a "mature" form of a polypeptide or protein may arise from a step of post-translational modification other than a proteolytic cleavage event. Such additional processes include, by way of non-limiting example, glycosylation, myristoylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or a combination of any of them.

2. active

[0055] An active AAP polypeptide or AAP polypeptide fragment retains a biological and/or an immunological activity similar, but not necessarily identical, to an activity of a naturally-occurring (wild-type) AAP polypeptide of the invention, including mature forms. A particular biological assay, with or without dose dependency, can be used to determine AAP activity. A nucleic acid fragment encoding a biologically-active portion of AAP can be prepared by isolating a portion of SEQ ID NO: 3 that encodes a polypeptide having an AAP biological activity (the biological activities of the AAP are described below), expressing the encoded portion of AAP (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of AAP. Immunological activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native AAP; biological activity refers to a function, either inhibitory or stimulatory, caused by a native AAP that excludes immunological activity.

AAP nucleic acid variants and hybridization

[0056] 1. *variant polynucleotides, genes and recombinant genes* The invention further encompasses nucleic acid molecules that differ from the nucleotide sequences shown in SEQ ID NO: 3, due to degeneracy of the genetic code and thus encode the same AAP as that encoded by the nucleotide sequences shown in SEQ ID NO: 3. An isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ ID NO: 4.

[0057] In addition to the AAP sequences shown in SEQ ID NO: 3, DNA sequence polymorphisms that change the amino acid sequences of the AAP may exist within a population. For example, allelic variation among individuals will exhibit genetic polymorphism in an AAP. The terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame (ORF) encoding an AAP, preferably a vertebrate AAP. Such natural allelic variations can typically result in 1-5% variance in an AAP. Any and all such nucleotide variations and resulting amino acid polymorphisms in an AAP, which are the result of natural allelic variation and that do not alter the functional activity of an AAP are within the scope of the invention.

[0058] Moreover, AAP from other species that have a nucleotide sequence that differs from the human sequence of SEQ ID NO: 3, are contemplated. Nucleic acid molecules corresponding to natural allelic variants and homologues of an AAP cDNAs of the invention can be isolated based on their homology to an AAP of SEQ ID NO: 3 using cDNA-derived probes to hybridize to homologous AAP sequences under stringent conditions.

[0059] "AAP variant polynucleotide" or "AAP variant nucleic acid sequence" means a nucleic acid molecule which encodes an active AAP that (1) has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native AAP, (2) a full-length native AAP lacking the signal peptide, (3) an extracellular domain of an AAP, with or without the signal peptide, or (4) any other fragment of a full-length AAP. Ordinarily, an AAP variant polynucleotide will have at least about 80% nucleic acid sequence identity, more preferably at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% nucleic acid sequence identity and yet more preferably at least about 99% nucleic acid sequence identity with the nucleic acid sequence encoding a full-length native AAP. An AAP variant polynucleotide may encode a full-length native AAP lacking the signal peptide, an extracellular domain of an AAP, with or without the signal sequence, or any other fragment of a full-length AAP. Variants do not encompass the native nucleotide sequence.

[0060] Ordinarily, AAP variant polynucleotides are at least about 30 nucleotides in length, often at least about 60, 90, 120, 150, 180, 210, 240, 270, 300, 450, 600 nucleotides in length, more often at least about 900 nucleotides in length, or more.

[0061] "Percent (%) nucleic acid sequence identity" with respect to AAP-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the AAP sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining % nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences

being compared.

[0062] When nucleotide sequences are aligned, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) can be calculated as follows:

$$\% \text{nucleic acid sequence identity} = W/Z \cdot 100$$

where

W is the number of nucleotides cored as identical matches by the sequence alignment program's or algorithm's alignment of C and D

and

Z is the total number of nucleotides in D.

[0063] When the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

2. Stringency

[0064] Homologs (*i.e.*, nucleic acids encoding an AAP derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

[0065] The specificity of single stranded DNA to hybridize complementary fragments is determined by the "stringency" of the reaction conditions. Hybridization stringency increases as the propensity to form DNA duplexes decreases. In nucleic acid hybridization reactions, the stringency can be chosen to either favor specific hybridizations (high stringency), which can be used to identify, for example, full-length clones from a library. Less-specific hybridizations (low stringency) can be used to identify related, but not exact, DNA molecules (homologous, but not identical) or segments.

[0066] DNA duplexes are stabilized by: (1) the number of complementary base pairs, (2) the type of base pairs, (3) salt concentration (ionic strength) of the reaction mixture, (4) the temperature of the reaction, and (5) the presence of certain organic solvents, such as formamide which decreases DNA duplex stability. In general, the longer the probe, the higher the temperature required for proper annealing. A common approach is to vary the temperature: higher relative temperatures result in more stringent reaction conditions. (Ausubel *et al.*, 1987) provide an excellent explanation of stringency of hybridization reactions.

[0067] To hybridize under "stringent conditions" describes hybridization protocols in which nucleotide sequences at least 60% homologous to each other remain hybridized. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m, 50% of the probes are occupied at equilibrium.

(a) high stringency

[0068] "Stringent hybridization conditions" conditions enable a probe, primer or oligonucleotide to hybridize only to its target sequence. Stringent conditions are sequence-dependent and will differ. Stringent conditions comprise: (1) low ionic strength and high temperature washes (*e.g.* 15 mM sodium chloride, 1.5 mM sodium citrate, 0.1 % sodium dodecyl sulfate at 50°C); (2) a denaturing agent during hybridization (*e.g.* 50% (v/v) formamide, 0.1% bovine serum albumin, 0.1% Ficoll, 0.1% polyvinylpyrrolidone, 50mM sodium phosphate buffer (pH 6.5; 750 mM sodium chloride, 75 mM sodium citrate at 42°C); or (3) 50% formamide. Washes typically also comprise 5X SSC (0.75 M NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. These conditions are presented as examples and are not meant to be limiting.

(b) *moderate stringency*

[0069] "Moderately stringent conditions" use washing solutions and hybridization conditions that are less stringent (Sambrook, 1989), such that a polynucleotide will hybridize to the entire, fragments, derivatives or analogs of SEQ ID NO: 3. One example comprises hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. The temperature, ionic strength, *etc.*, can be adjusted to accommodate experimental factors such as probe length. Other moderate stringency conditions are described in (Ausubel *et al.*, 1987; Kriegler, 1990).

(c) *low stringency*

[0070] "Low stringent conditions" use washing solutions and hybridization conditions that are less stringent than those for moderate stringency (Sambrook, 1989), such that a polynucleotide will hybridize to the entire, fragments, derivatives or analogs of SEQ ID NO: 3. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency, such as those for cross-species hybridizations are described in (Ausubel *et al.*, 1987; Kriegler, 1990; Shilo and Weinberg, 1981).

3. *Conservative mutations*

[0071] In addition to naturally-occurring allelic variants of AAP, changes can be introduced by mutation into SEQ ID NO: 3 sequences that incur alterations in the amino acid sequences of the encoded AAP that do not alter the AAP function. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of SEQ ID NO: 4. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequences of the AAP without altering their biological activity, whereas an "essential" amino acid residue is required for such biological activity. For example, amino acid residues that are conserved among the AAP of the invention are predicted to be particularly non-amenable to alteration. Amino acids for which conservative substitutions can be made are well-known in the art.

[0072] Useful conservative substitutions are shown in Table A, "Preferred substitutions." Conservative substitutions whereby an amino acid of one class is replaced with another amino acid of the same type fall within the scope of the subject invention so long as the substitution does not materially alter the biological activity of the compound. If such substitutions result in a change in biological activity, then more substantial changes, indicated in Table B as exemplary are introduced and the products screened for an AAP polypeptide's biological activity.

Table A Preferred substitutions

Original residue	Exemplary substitutions	Preferred substitutions
Ala (A)	Val, Leu, Ile	Val
Arg (R)	Lys, Gln, Asn	Lys
Asn (N)	Gln, His, Lys, Arg	Gln
Asp (D)	Glu	Glu
Cys (C)	Ser	Ser
Gln (Q)	Asn	Asn
Glu (E)	Asp	Asp
Gly (G)	Pro, Ala	Ala
His (H)	Asn, Gln, Lys, Arg	Arg
Ile (I)	Leu, Val, Met, Ala, Phe, Norleucine	Leu
Leu (L)	Norleucine, Ile, Val, Met, Ala, Phe	Ile
Lys (K)	Arg, Gln, Asn	Arg
Met (M)	Leu, Phe, Ile	Leu
Phe (F)	Leu, Val, Ile, Ala, Tyr	Leu

(continued)

Original residue	Exemplary substitutions	Preferred substitutions
Pro (P)	Ala	Ala
Ser (S)	Thr	Thr
Thr (T)	Ser	Ser
Trp (W)	Tyr, Phe	Tyr
Tyr (Y)	Trp, Phe, Thr, Ser	Phe
Val (V)	Ile, Leu, Met, Phe, Ala, Norleucine	Leu

[0073] Non-conservative substitutions that effect (1) the structure of the polypeptide backbone, such as a β -sheet or α -helical conformation, (2) the charge or (3) hydrophobicity, or (4) the bulk of the side chain of the target site can modify an AAP polypeptide's function or immunological identity. Residues are divided into groups based on common side-chain properties as denoted in Table B. Non-conservative substitutions entail exchanging a member of one of these classes for another class. Substitutions may be introduced into conservative substitution sites or more preferably into non-conserved sites.

Table B Amino acid classes

Class	Amino acids
hydrophobic	Norleucine, Met, Ala, Val, Leu, Ile
neutral hydrophilic	Cys, Ser, Thr
acidic	Asp, Glu
basic	Asn, Gln, His, Lys, Arg
disrupt chain conformation	Gly, Pro
aromatic	Trp, Tyr, Phe

[0074] The variant polypeptides can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis (Carter, 1986; Zoller and Smith, 1987), cassette mutagenesis, restriction selection mutagenesis (Wells *et al.*, 1985) or other known techniques can be performed on the cloned DNA to produce the AAP variant DNA (Ausubel *et al.*, 1987; Sambrook, 1989).

[0075] In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 45%, preferably 60%, more preferably 70%, 80%, 90%, and most preferably about 95% homologous to SEQ ID NO: 3.

[0076] A mutant AAP can be assayed for blocking angiogenesis *in vitro*.

4. Anti-sense nucleic acids

[0077] Using antisense and sense AAP oligonucleotides can prevent AAP polypeptide expression. These oligonucleotides bind to target nucleic acid sequences, forming duplexes that block transcription or translation of the target sequence by enhancing degradation of the duplexes, terminating prematurely transcription or translation, or by other means.

[0078] Antisense or sense oligonucleotides are single-stranded nucleic acids, either RNA or DNA, which can bind a target AAP mRNA (sense) or an AAP DNA (antisense) sequences. Anti-sense nucleic acids can be designed according to Watson and Crick or Hoogsteen base pairing rules. The anti-sense nucleic acid molecule can be complementary to the entire coding region of an AAP mRNA, but more preferably, to only a portion of the coding or noncoding region of an AAP mRNA. For example, the anti-sense oligonucleotide can be complementary to the region surrounding the translation start site of an AAP mRNA. Antisense or sense oligonucleotides may comprise a fragment of the AAP DNA coding region of at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. In general, antisense RNA or DNA molecules can comprise at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 bases in length or more. Among others, (Stein and Cohen, 1988; van der Krol *et al.*, 1988a) describe methods to derive antisense or a sense oligonucleotides from a given cDNA sequence.

[0079] Examples of modified nucleotides that can be used to generate the anti-sense nucleic acid include: 5-fluorouracil,

5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine; 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the anti-sense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been sub-

cloned in an anti-sense orientation such that the transcribed RNA will be complementary to a target nucleic acid of interest. **[0080]** To introduce antisense or sense oligonucleotides into target cells (cells containing the target nucleic acid sequence), any gene transfer method may be used. Examples of gene transfer methods include (1) biological, such as gene transfer vectors like Epstein-Barr virus or conjugating the exogenous DNA to a ligand-binding molecule, (2) physical, such as electroporation and injection, and (3) chemical, such as CaPO_4 precipitation and oligonucleotide-lipid complexes.

[0081] An antisense or sense oligonucleotide is inserted into a suitable gene transfer retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Examples of suitable retroviral vectors include those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (WO 90/13641, 1990). To achieve sufficient nucleic acid molecule transcription, vector constructs in which the transcription of the anti-sense nucleic acid molecule is controlled by a strong pol II or pol III promoter are preferred.

[0082] To specify target cells in a mixed population of cells cell surface receptors that are specific to the target cells can be exploited. Antisense and sense oligonucleotides are conjugated to a ligand-binding molecule, as described in (WO 91/04753, 1991). Ligands are chosen for receptors that are specific to the target cells. Examples of suitable ligand-binding molecules include cell surface receptors, growth factors, cytokines, or other ligands that bind to cell surface receptors or molecules. Preferably, conjugation of the ligand-binding molecule does not substantially interfere with the ability of the receptors or molecule to bind the ligand-binding molecule conjugate, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

[0083] Liposomes efficiently transfer sense or an antisense oligonucleotide to cells (WO 90/10448, 1990). The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

[0084] The anti-sense nucleic acid molecule of the invention may be an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual α -units, the strands run parallel to each other (Gautier *et al.*, 1987). The anti-sense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.*, 1987a) or a chimeric RNA-DNA analogue (Inoue *et al.*, 1987b).

[0085] In one embodiment, an anti-sense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes, such as hammerhead ribozymes (Haseloff and Gerlach, 1988) can be used to catalytically cleave AAP mRNA transcripts and thus inhibit translation. A ribozyme specific for an AAP-encoding nucleic acid can be designed based on the nucleotide sequence of an AAP cDNA (*i.e.*, SEQ ID NO: 3). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an AAP-encoding mRNA (Cech *et al.*, U.S. Patent No. 5,116,742, 1992; Cech *et al.*, U.S. Patent No. 4,987,071, 1991). An AAP mRNA can also be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules (Bartel and Szostak, 1993).

[0086] Alternatively, AAP expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an AAP (*e.g.*, an AAP promoter and/or enhancers) to form triple helical structures that prevent transcription of an AAP in target cells (Helene, 1991; Helene *et al.*, 1992; Maher, 1992).

[0087] Modifications of antisense and sense oligonucleotides can augment their effectiveness. Modified sugar-phosphodiester bonds or other sugar linkages (WO 91/06629, 1991), increase *in vivo* stability by conferring resistance to endogenous nucleases without disrupting binding specificity to target sequences. Other modifications can increase the affinities of the oligonucleotides for their targets, such as covalently linked organic moieties (WO 90/10448, 1990) or poly-(L)-lysine. Other attachments modify binding specificities of the oligonucleotides for their targets, including metal complexes or intercalating (*e.g.* ellipticine) and alkylating agents.

[0088] For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (Hyrup and Nielsen, 1996). "Peptide nucleic acids" or "PNAs" refer to nucleic acid mimics (*e.g.*, DNA mimics) in that the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs allows for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols (Hyrup and Nielsen, 1996; Perry-O'Keefe *et al.* 1996).

[0089] PNAs of an AAP can be used in therapeutic and diagnostic applications. For example, PNAs can be used as

anti-sense or antigene agents for sequence-specific modulation of gene expression by inducing transcription or translation arrest or inhibiting replication. AAP PNAs may also be used in the analysis of single base pair mutations (*e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S₁ nucleases (Hyrup and Nielsen, 1996); or as probes or primers for DNA sequence and hybridization (Hyrup and Nielsen, 1996; Perry-O'Keefe *et al.*, 1996).

[0090] PNAs of an AAP can be modified to enhance their stability or cellular uptake. Lipophilic or other helper groups may be attached to PNAs, PNA-DNA dimmers formed, or the use of liposomes or other drug delivery techniques. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes (*e.g.*, RNase H and DNA polymerases) to interact with the DNA portion while the PNA portion provides high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup and Nielsen, 1996). The synthesis of PNA-DNA chimeras can be performed (Finn *et al.*, 1996; Hyrup and Nielsen, 1996). For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Finn *et al.*, 1996; Hyrup and Nielsen, 1996). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.*, 1996). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment (Petersen *et al.*, 1976).

[0091] The oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (Lemaitre *et al.*, 1987; Letsinger *et al.*, 1989) or PCT Publication No. WO88/09810) or the blood-brain barrier (*e.g.*, PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (van der Krol *et al.*, 1988b) or intercalating agents (Zon, 1988). The oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, and the like.

AAP polypeptides

[0092] One aspect of the invention pertains to isolated AAP, and biologically-active portions derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-AAP Abs. In one embodiment, a native AAP can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, AAP are produced by recombinant DNA techniques. Alternative to recombinant expression, an AAP can be synthesized chemically using standard peptide synthesis techniques.

1. Polypeptides

[0093] An AAP polypeptide includes the amino acid sequence of an AAP whose sequences are provided in SEQ ID NO: 4. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residues shown in SEQ ID NO: 4, while still encoding a protein that maintains its AAP activities and physiological functions, or a functional fragment thereof

2. Variant AAP polypeptides

[0094] In general, an AAP variant that preserves an AAP-like function and includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further includes the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

[0095] 90% "AAP polypeptide variant" means an active AAP polypeptide having at least: (1) about amino acid sequence identity with a full-length native sequence AAP polypeptide sequence, (2) an AAP polypeptide sequence lacking the signal peptide, (3) an extracellular domain of an AAP polypeptide, with or without the signal peptide, or (4) any other fragment of a full-length AAP polypeptide sequence. For example, AAP polypeptide variants include AAP polypeptides wherein one or more amino acid residues are added or deleted at the N- or C- terminus of the full-length native amino acid sequence. An AAP polypeptide variant will have at least about 90% amino acid sequence identity, preferably at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% amino acid sequence identity and most preferably at least about 99% amino acid sequence identity with a full-length native sequence AAP polypeptide sequence. An AAP polypeptide variant may have a sequence lacking the signal peptide, an extracellular domain of an AAP polypeptide, with or without the signal peptide, or any other fragment of a full-length AAP polypeptide sequence. Ordinarily, AAP variant polypeptides are at least about 10 amino acids in length, often at least about 20 amino acids in length, more often at least about 30,

40, 50, 60, 70, 80, 90, 100, 150, 200, or 300 amino acids in length, or more.

[0096] "Percent (%) amino acid sequence identity" is defined as the percentage of amino acid residues that are identical with amino acid residues in a disclosed AAP polypeptide sequence in a candidate sequence when the two sequences are aligned. To determine % amino acid identity, sequences are aligned and if necessary, gaps are introduced to achieve the maximum % sequence identity, conservative substitutions are not considered as part of the sequence identity. Amino acid sequence alignment procedures to determine percent identity are well known to those of skill in the art. Often publicly available computer software such as BLAST, BLAST2, ALIGN2 or Megalign (DNASTAR) software is used to align peptide sequences. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

[0097] When amino acid sequences are aligned, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) can be calculated as:

$$\% \text{amino acid sequence identity} = X/Y \cdot 100$$

where

X is the number of amino acid residues scored as identical matches by the sequence alignment program's or algorithm's alignment of A and B

and

Y is the total number of amino acid residues in B.

[0098] If the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

3. Isolated/purified polypeptides

[0099] An "isolated" or "purified" polypeptide, protein or biologically active fragment is separated and/or recovered from a component of its natural environment. Contaminant components include materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous materials. Preferably, the polypeptide is purified to a sufficient degree to obtain at least 15 residues of N-terminal or internal amino acid sequence. To be substantially isolated, preparations having less than 30% by dry weight of non-AAP contaminating material (contaminants), more preferably less than 20%, 10% and most preferably less than 5% contaminants. An isolated, recombinantly-produced AAP or biologically active portion is preferably substantially free of culture medium, *i.e.*, culture medium represents less than 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the AAP preparation. Examples of contaminants include cell debris, culture media, and substances used and produced during *in vitro* synthesis of an AAP.

4. Biologically active

[0100] Biologically active portions of an AAP include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequences of an AAP (SEQ ID NO: 4) that include fewer amino acids than a full-length AAP, and exhibit at least one activity of an AAP. Biologically active portions comprise a domain or motif with at least one activity of a native AAP. A biologically active portion of an AAP can be a polypeptide that is, for example, 10, 25, 50, 100 or more amino acid residues in length. Other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native AAP.

[0101] Biologically active portions of an AAP may have an amino acid sequence shown in SEQ ID NO: 4, or substantially homologous to SEQ ID NO: 4, and retains the functional activity of the protein of SEQ ID NO: 4, yet differs in amino acid sequence due to natural allelic variation or mutagenesis. Other biologically active AAP may comprise an amino acid sequence at least 45% homologous to the amino acid sequence of SEQ ID NO: 4, and retains the functional activity of native AAP.

5. Determining homology between two or more sequences

[0102] "AAP variant" means an active AAP having at least: (1) about 80% amino acid sequence identity with a full-length native sequence AAP sequence, (2) an AAP sequence lacking the signal peptide, (3) an extracellular domain of

an AAP, with or without the signal peptide, or (4) any other fragment of a full-length AAP sequence. For example, AAP variants include an AAP wherein one or more amino acid residues are added or deleted at the N- or C- terminus of the full-length native amino acid sequence. An AAP variant will have at least about 80% amino acid sequence identity, preferably at least about 81% amino acid sequence identity, more preferably at least about 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% amino acid sequence identity and most preferably at least about 99% amino acid sequence identity with a full-length native sequence AAP sequence. An AAP variant may have a sequence lacking the signal peptide, an extracellular domain of an AAP, with or without the signal peptide, or any other fragment of a full-length AAP sequence. Ordinarily, AAP variant polypeptides are at least about 10 amino acids in length, often at least about 20 amino acids in length, more often at least about 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, or 300 amino acids in length, or more.

[0103] "Percent (%) amino acid sequence identity" is defined as the percentage of amino acid residues that are identical with amino acid residues in a disclosed AAP sequence in a candidate sequence when the two sequences are aligned. To determine % amino acid identity, sequences are aligned and if necessary, gaps are introduced to achieve the maximum % sequence identity; conservative substitutions are not considered as part of the sequence identity. Amino acid sequence alignment procedures to determine percent identity are well known to those of skill in the art. Often publicly available computer software such as BLAST, BLAST2, ALIGN2 or Megalign (DNASTAR) software is used to align peptide sequences. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

[0104] When amino acid sequences are aligned, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) can be calculated as:

$$\% \text{amino acid sequence identity} = X/Y \cdot 100$$

where

X is the number of amino acid residues scored as identical matches by the sequence alignment program's or algorithm's alignment of A and B

and

Y is the total number of amino acid residues in B.

[0105] If the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

6. Chimeric and fusion proteins

[0106] Fusion polypeptides are useful in expression studies, cell-localization, bioassays, and AAP purification. An AAP "chimeric protein" or "fusion protein" comprises an AAP fused to a non-AAP polypeptide. A non-AAP polypeptide is not substantially homologous to an AAP (SEQ ID NO: 4). An AAP fusion protein may include any portion to an entire AAP, including any number of the biologically active portions. An AAP may be fused to the C-terminus of the GST (glutathione S-transferase) sequences. Such fusion proteins facilitate the purification of a recombinant AAP. In certain host cells, (e.g. mammalian), heterologous signal sequences fusions may ameliorate AAP expression and/or secretion. Additional exemplary fusions are presented in Table C.

[0107] Other fusion partners can adapt an AAP therapeutically. Fusions with members of the immunoglobulin (Ig) protein family are useful in therapies that inhibit an AAP ligand or substrate interactions, consequently suppressing an AAP-mediated signal transduction *in vivo*. Such fusions, incorporated into pharmaceutical compositions, may be used to treat proliferative and differentiation disorders, as well as modulating cell survival. An AAP-Ig fusion polypeptides can also be used as immunogens to produce an anti-AAP Abs in a subject, to purify AAP ligands, and to screen for molecules that inhibit interactions of an AAP with other molecules.

[0108] Fusion proteins can be easily created using recombinant methods. A nucleic acid encoding an AAP can be fused in-frame with a non-AAP encoding nucleic acid, to an AAP NH₂- or COO- -terminus, or internally. Fusion genes may also be synthesized by conventional techniques, including automated DNA synthesizers. PCR amplification using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (Ausubel *et al.*, 1987) is also useful. Many vectors are commercially available that facilitate sub-cloning an AAP in-frame to a fusion moiety.

Table C Useful non-AAP fusion polypeptides

Reporter	<i>in vitro</i>	<i>in vivo</i>	Notes	Reference
Human growth hormone (hGH)	Radioimmuno-assay	none	Expensive, insensitive, narrow linear range.	(Selden <i>et al.</i> , 1986)
β -glucuronidase (GUS)	Colorimetric, fluorescent, or chemiluminescent	colorimetric (histochemical staining with X- gluc)	sensitive, broad linear range, non-iostopic.	(Gallagher, 1992)
Green fluorescent protein (GFP) and related molecules (RFP, BFP, AAP, <i>etc.</i>)	Fluorescent	fluorescent '	can be used in live cells; resists photo-bleaching	(Chalfie <i>et al.</i> , 1994)
Luciferase (firefly)	bioluminescent	Bio-luminescent	protein is unstable, difficult to reproduce, signal is brief	(de Wet <i>et al.</i> , 1987)
Chloramphenicol acetyltransferase (CAT)	Chromatography, differential extraction, fluorescent, or immunoassay	none	Expensive radioactive substrates, time-consuming, insensitive, narrow linear range	(Gorman <i>et al.</i> , 1982)
β -galactosidase	colorimetric, fluorescence, chemiluminescence	colorimetric (histochemical staining with X-gal), bio-luminescent in live cells	sensitive, broad linear range; some cells have high endogenous activity	(Alam and Cook, 1990)
Secreted alkaline phosphatase (SEAP)	colorimetric, bioluminescent, chemiluminescent	none	Chemiluminescence assay is sensitive and broad linear range; some cells have endogenous alkaline phosphatase activity	(Berger <i>et al.</i> , 1988)

Therapeutic applications of AAP

1. Agonists and antagonists

[0109] "Antagonist" includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of an endogenous AAP. Similarly, "agonist" includes any molecule that mimics a biological activity of an endogenous AAP. Molecules that can act as agonists or antagonists include Abs or antibody fragments, fragments or variants of an endogenous AAP, peptides, antisense oligonucleotides, small organic molecules, *etc.*

2. Identifying antagonists and agonists

[0110] To assay for antagonists, an AAP is added to, or expressed in, a cell along with the compound to be screened for a particular activity. If the compound inhibits the activity of interest in the presence of an AAP, that compound is an antagonist to the AAP; if an AAP activity is enhanced, the compound is an agonist.

(a) *Specific examples of potential antagonists and agonist*

[0111] Any molecule that alters AAP cellular effects is a candidate antagonist or agonist. Screening techniques well known to those skilled in the art can identify these molecules. Examples of antagonists and agonists include: (1) small organic and inorganic compounds, (2) small peptides, (3) Abs and derivatives, (4) polypeptides closely related to an AAP, (5) antisense DNA and RNA, (6) ribozymes, (7) triple DNA helices and (8) nucleic acid aptamers.

[0112] Small molecules that bind to an AAP active site or other relevant part of the polypeptide and inhibit the biological activity of the AAP are antagonists. Examples of small molecule antagonists include small peptides, peptide-like molecules, preferably soluble, and synthetic non-peptidyl organic or inorganic compounds. These same molecules, if they enhance an AAP activity, are examples of agonists.

[0113] Almost any antibody that affects an AAP's function is a candidate antagonist, and occasionally, agonist. Examples of antibody antagonists include polyclonal, monoclonal, single-chain, anti-idiotypic, chimeric Abs, or humanized versions of such Abs or fragments. Abs may be from any species in which an immune response can be raised. Humanized Abs are also contemplated.

[0114] Alternatively, a potential antagonist or agonist may be a closely related protein, for example, a mutated form of an AAP that recognizes an AAP-interacting protein but imparts no effect, thereby competitively inhibiting AAP action. Alternatively, a mutated AAP may be constitutively activated and may act as an agonist.

[0115] Antisense RNA or DNA constructs can be effective antagonists. Antisense RNA or DNA molecules block function by inhibiting translation by hybridizing to targeted mRNA. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which depend on polynucleotide binding to DNA or RNA. For example, the 5' coding portion of an AAP sequence is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix) (Beal and Dervan, 1991; Cooney *et al.*, 1988; Lee *et al.*, 1979), thereby preventing transcription and the production of the AAP. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the AAP (antisense) (Cohen, 1989; Okano *et al.*, 1991). These oligonucleotides can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the AAP. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, *e.g.*, between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

[0116] Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques (WO 97/33551, 1997; Rossi, 1994).

[0117] To inhibit transcription, triple-helix nucleic acids that are single-stranded and comprise deoxynucleotides are useful antagonists. These oligonucleotides are designed such that triple-helix formation via Hoogsteen base-pairing rules is promoted, generally requiring stretches of purines or pyrimidines (WO 97/33551, 1997).

[0118] Aptamers are short oligonucleotide sequences that can be used to recognize and specifically bind almost any molecule. The systematic evolution of ligands by exponential enrichment (SELEX) process (Ausubel *et al.*, 1987; Ellington and Szostak, 1990; Tuerk and Gold, 1990) is powerful and can be used to find such aptamers. Aptamers have many diagnostic and clinical uses; almost any use in which an antibody has been used clinically or diagnostically, aptamers too may be used. In addition, they are cheaper to make once they have been identified, and can be easily applied in a variety of formats, including administration in pharmaceutical compositions, in bioassays, and diagnostic tests (Jayasena, 1999).

Anti-AAP Abs

[0119] The invention encompasses Abs and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any AAP epitopes.

[0120] "Antibody" (Ab) comprises single Abs directed against an AAP (anti-AAP Ab; including agonist, antagonist, and neutralizing Abs), anti-AAP Ab compositions with poly-epitope specificity, single chain anti-AAP Abs, and fragments of anti-AAP Abs. A "monoclonal antibody" is obtained from a population of substantially homogeneous Abs, *i.e.*, the individual Abs comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts. Exemplary Abs include polyclonal (pAb), monoclonal (mAb), humanized, bi-specific (bsAb), and heteroconjugate Abs.

1. Polyclonal Abs (pAbs)

[0121] Polyclonal Abs can be raised in a mammalian host, for example, by one or more injections of an immunogen and, if desired, an adjuvant. Typically, the immunogen and/or adjuvant are injected in the mammal by multiple subcu-

taneous or intraperitoneal injections. The immunogen may include an AAP or a fusion protein. Examples of adjuvants include Freund's complete and monophosphoryl Lipid A synthetic-trehalose dicorynomycolate (MPL-TDM). To improve the immune response, an immunogen may be conjugated to a protein that is immunogenic in the host, such as keyhole limpet hemocyanin (KLH), serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Protocols for antibody production are described by (Ausubel *et al.*, 1987; Harlow and Lane, 1988). Alternatively, pAbs may be made in chickens, producing IgY molecules (Schade *et al.*, 1996).

2. Monoclonal Abs (mAbs)

[0122] Anti-AAP mAbs may be prepared using hybridoma methods (Milstein and Cuello, 1983). Hybridoma methods comprise at least four steps: (1) immunizing a host, or lymphocytes from a host; (2) harvesting the mAb secreting (or potentially secreting) lymphocytes, (3) fusing the lymphocytes to immortalized cells, and (4) selecting those cells that secrete the desired (anti-AAP) mAb.

[0123] A mouse, rat, guinea pig, hamster, or other appropriate host is immunized to elicit lymphocytes that produce or are capable of producing Abs that will specifically bind to the immunogen. Alternatively, the lymphocytes may be immunized *in vitro*. If human cells are desired, peripheral blood lymphocytes (PBLs) are generally used; however, spleen cells or lymphocytes from other mammalian sources are preferred. The immunogen typically includes an AAP or a fusion protein.

[0124] The lymphocytes are then fused with an immortalized cell line to form hybridoma cells, facilitated by a fusing agent such as polyethylene glycol (Goding, 1996). Rodent, bovine, or human myeloma cells immortalized by transfection may be used, or rat or mouse myeloma cell lines. Because pure populations of hybridoma cells and not unfused immortalized cells are preferred, the cells after fusion are grown in a suitable medium that contains one or more substances that inhibit the growth or survival of unfused, immortalized cells. A common technique uses parental cells that lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or BPRT). In this case, hypoxanthine, aminopterin and thymidine are added to the medium (HAT medium) to prevent the growth of HGPRT-deficient cells while permitting hybridomas to grow.

[0125] Preferred immortalized cells fuse efficiently, can be isolated from mixed populations by selecting in a medium such as HAT, and support stable and high-level expression of antibody after fusion. Preferred immortalized cell lines are murine myeloma lines, available from the American Type Culture Collection (Manassas, VA). Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human mAbs (Kozbor *et al.*, 1984; Schook, 1987).

[0126] Because hybridoma cells secrete antibody extracellularly, the culture media can be assayed for the presence of mAbs directed against an AAP (anti-AAP mAbs). Immunoprecipitation or *in vitro* binding assays, such as radio immunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA), measure the binding specificity of mAbs (Harlow and Lane, 1988; Harlow and Lane, 1999), including Scatchard analysis (Munson and Rodbard, 1980).

[0127] Anti-AAP mAb secreting hybridoma cells may be isolated as single clones by limiting dilution procedures and sub-cultured (Goding, 1996). Suitable culture media include Dulbecco's Modified Eagle's Medium, RPMI-1640, or if desired, a protein-free or -reduced or serum-free medium (*e.g.*, Ultra DOMA PF or HL-1; Biowhittaker; Walkersville, MD). The hybridoma cells may also be grown *in vivo* as ascites.

[0128] The mAbs may be isolated or purified from the culture medium or ascites fluid by conventional Ig purification procedures such as protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, ammonium sulfate precipitation or affinity chromatography (Harlow and Lane, 1988; Harlow and Lane, 1999).

[0129] The mAbs may also be made by recombinant methods (U.S. Patent No. 4166452, 1979). DNA encoding anti-AAP mAbs can be readily isolated and sequenced using conventional procedures, *e.g.*, using oligonucleotide probes that specifically bind to murine heavy and light antibody chain genes, to probe preferably DNA isolated from anti-AAP-secreting mAb hybridoma cell lines. Once isolated, the isolated DNA fragments are sub-cloned into expression vectors that are then transfected into host cells such as simian COS-7 cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce Ig protein, to express mAbs. The isolated DNA fragments can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4816567, 1989; Morrison *et al.*, 1987), or by fusing the Ig coding sequence to all or part of the coding sequence for a non-Ig polypeptide. Such a non-Ig polypeptide can be substituted for the constant domains of an antibody, or can be substituted for the variable domains of one antigen-combining site to create a chimeric bivalent antibody.

3. Monovalent Abs

[0130] The Abs may be monovalent Abs that consequently do not cross-link with each other. For example, one method involves recombinant expression of Ig light chain and modified heavy chain. Heavy chain truncations generally at any

point in the F_c region will prevent heavy chain cross-linking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted, preventing crosslinking. *In vitro* methods are also suitable for preparing monovalent Abs. Abs can be digested to produce fragments, such as F_{ab} fragments (Harlow and Lane, 1988; Harlow and Lane, 1999).

4. Humanized and human Abs

[0131] Anti-AAP Abs may further comprise humanized or human Abs. Humanized forms of non-human Abs are chimeric Igs, Ig chains or fragments (such as F_v , F_{ab} , $F_{ab'}$, $F_{(ab')_2}$ or other antigen-binding subsequences of Abs) that contain minimal sequence derived from non-human Ig.

[0132] Generally, a humanized antibody has one or more amino acid residues introduced from a non-human source. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization is accomplished by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody (Jones *et al.*, 1986; Riechmann *et al.*, 1988; Verhoeyen *et al.*, 1988). Such "humanized" Abs are chimeric Abs (U.S. Patent No. 4816567, 1989), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized Abs are typically human Abs in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent Abs. Humanized Abs include human Igs (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit, having the desired specificity, affinity and capacity. In some instances, corresponding non-human residues replace F_v framework residues of the human Ig. Humanized Abs may comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody comprises substantially all of at least one, and typically two, variable domains, in which most if not all of the CDR regions correspond to those of a non-human Ig and most if not all of the FR regions are those of a human Ig consensus sequence. The humanized antibody optimally also comprises at least a portion of an Ig constant region (F_c), typically that of a human Ig (Jones *et al.*, 1986; Presta, 1992; Riechmann *et al.*, 1988).

[0133] Human Abs can also be produced using various techniques, including phage display libraries (Hoogenboom *et al.*, 1991; Marks *et al.*, 1991) and the preparation of human mAbs (Boerner *et al.*, 1991; Reisfeld and Sell, 1985). Similarly, introducing human Ig genes into transgenic animals in which the endogenous Ig genes have been partially or completely inactivated can be exploited to synthesize human Abs. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire (U.S. Patent No. 5545807, 1996; U.S. Patent No. 5545806, 1996; U.S. Patent No. 5569825, 1996; U.S. Patent No. 5633425, 1997; U.S. Patent No. 5661016, 1997; U.S. Patent No. 5625126, 1997; Fishwild *et al.*, 1996; Lonberg and Huszar, 1995; Lonberg *et al.*, 1994; Marks *et al.*, 1992).

5. Bi-specific mAbs

[0134] Bi-specific Abs are monoclonal, preferably human or humanized, that have binding specificities for at least two different antigens. For example, a binding specificity is an AAP; the other is for any antigen of choice, preferably a cell-surface protein or receptor or receptor subunit.

[0135] Traditionally, the recombinant production of bi-specific Abs is based on the co-expression of two Ig heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, 1983). Because of the random assortment of Ig heavy and light chains, the resulting hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the desired bi-specific structure. The desired antibody can be purified using affinity chromatography or other techniques (WO 93/08829, 1993; Traunecker *et al.*, 1991).

[0136] To manufacture a bi-specific antibody (Suresh *et al.*, 1986), variable domains with the desired antibody-antigen combining sites are fused to Ig constant domain sequences. The fusion is preferably with an Ig heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. Preferably, the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding is in at least one of the fusions. DNAs encoding the Ig heavy-chain fusions and, if desired, the Ig light chain, are inserted into separate expression vectors and are co-transfected into a suitable host organism.

[0137] The interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers that are recovered from recombinant cell culture (WO 96/27011, 1996). The preferred interface comprises at least part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This mechanism increases the yield of the heterodimer over unwanted end products such as homodimers.

[0138] Bi-specific Abs can be prepared as full length Abs or antibody fragments (e.g. $F_{(ab')_2}$ bi-specific Abs). One technique to generate bi-specific Abs exploits chemical linkage. Intact Abs can be proteolytically cleaved to generate $F_{(ab')_2}$ fragments (Brennan *et al.*, 1985). Fragments are reduced with a dithiol complexing agent, such as sodium arsenite, to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The generated $F_{ab'}$ fragments are then converted to thionitrobenzoate (TNB) derivatives. One of the $F_{ab'}$ -TNB derivatives is then reconverted to the $F_{ab'}$ -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other $F_{ab'}$ -TNB derivative to form the bi-specific antibody. The produced bi-specific Abs can be used as agents for the selective immobilization of enzymes.

[0139] $F_{ab'}$ fragments may be directly recovered from *E. coli* and chemically coupled to form bi-specific Abs. For example, fully humanized bi-specific $F_{(ab')_2}$ Abs can be produced (Shalaby *et al.*, 1992). Each $F_{ab'}$ fragment is separately secreted from *E. coli* and directly coupled chemically *in vitro*, forming the bi-specific antibody.

[0140] Various techniques for making and isolating bi-specific antibody fragments directly from recombinant cell culture have also been described. For example, leucine zipper motifs can be exploited (Kostelny *et al.*, 1992). Peptides from the *Fos* and *Jun* proteins are linked to the $F_{ab'}$ portions of two different Abs by gene fusion. The antibody homodimers are reduced at the hinge region to form monomers and then re-oxidized to form antibody heterodimers. This method can also produce antibody homodimers. The "diabody" technology (Holliger *et al.*, 1993) provides an alternative method to generate bi-specific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker that is too short to allow pairing between the two domains on the same chain. The V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, forming two antigen-binding sites. Another strategy for making bi-specific antibody fragments is the use of single-chain F_v (sF_v) dimers (Gruber *et al.*, 1994). Abs with more than two valencies are also contemplated, such as tri-specific Abs (Tutt *et al.*, 1991).

[0141] Exemplary bi-specific Abs may bind to two different epitopes on a given AAP. Alternatively, cellular defense mechanisms can be restricted to a particular cell expressing the particular AAP: an anti-AAP arm may be combined with an arm that binds to a leukocyte triggering molecule, such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or to F_c receptors for IgG ($F_c\gamma R$), such as $F_c\gamma RI$ (CD64), $F_c\gamma RII$ (CD32) and $F_c\gamma RIII$ (CD 16). Bi-specific Abs may also be used to target cytotoxic agents to cells that express a particular AAP. These Abs possess an AAP-binding arm and an arm that binds a cytotoxic agent or a radionuclide chelator.

6. Heteroconjugate Abs

[0142] Heteroconjugate Abs, consisting of two covalently joined Abs, have been proposed to target immune system cells to unwanted cells (4,676,980, 1987) and for treatment of human immunodeficiency virus (HIV) infection (WO 91/00360, 1991; WO 92/20373, 1992). Abs prepared *in vitro* using synthetic protein chemistry methods, including those involving cross-linking agents, are contemplated. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents include iminothiolate and methyl-4-mercaptobutyrimidate (4,676,980, 1987).

7. Immunoconjugates

[0143] Immunoconjugates may comprise an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin or fragment of bacterial, fungal, plant, or animal origin), or a radioactive isotope (i.e., a radioconjugate).

[0144] Useful enzymatically-active toxins and fragments include Diphtheria A chain, non-binding active fragments of Diphtheria toxin, exotoxin A chain from *Pseudomonas aeruginosa*, ricin A chain, abrin A chain, modeccin A chain, α -sarcin, *Aleurites fordii* proteins, Dianthin proteins, *Phytolacca americana* proteins, *Momordica charantia* inhibitor, curcin, crotin, *Sapaonaria officinalis* inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated Abs, such as ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

[0145] Conjugates of the antibody and cytotoxic agent are made using a variety of bi-functional protein-coupling agents, such as N-succinimidyl-3-(2-pyridylthiol) propionate (SPDP), iminothiolane (IT), bi-functional derivatives of imidoesters (such as dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazobenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared (Vitetta *et al.*, 1987). ^{14}C -labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugating radionuclide to antibody (WO 94/11026, 1994).

[0146] In another embodiment, the antibody may be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pre-targeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a streptavidin "ligand" (e.g.,

biotin) that is conjugated to a cytotoxic agent (*e.g.*, a radionuclide).

8. Effector function engineering

- 5 **[0147]** The antibody can be modified to enhance its effectiveness in treating a disease, such as cancer. For example, cysteine residue(s) may be introduced into the F_c region, thereby allowing interchain disulfide bond formation in this region. Such homodimeric Abs may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC) (Caron *et al.*, 1992; Shopes, 1992). Homodimeric Abs with enhanced anti-tumor activity can be prepared using hetero-bifunctional cross-linkers (Wolff *et al.*, 1993). Alternatively, 10 an antibody engineered with dual F_c regions may have enhanced complement lysis (Stevenson *et al.*, 1989).

9. Immunoliposomes

- 15 **[0148]** Liposomes containing the antibody may also be formulated (U.S. Patent No. 4485045, 1984; U.S. Patent No. 4544545, 1985; U.S. Patent No. 5013556, 1991; Eppstein *et al.*, 1985; Hwang *et al.*, 1980). Useful liposomes can be generated by a reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG- PE). Such preparations are extruded through filters of defined pore size to yield liposomes with a desired diameter. F_{ab} fragments of the antibody can be conjugated to the liposomes (Martin and Papahadjopoulos, 1982) via a disulfide-interchange reaction. A chemotherapeutic agent, such as Doxorubicin, may also be contained in the liposome (Gabizon *et al.*, 1989). Other useful liposomes with different compositions are contemplated. 20

10. Diagnostic applications of Abs directed against an AAP

- 25 **[0149]** Anti-AAP Abs can be used to localize and/or quantitate an AAP (*e.g.*, for use in measuring levels of an AAP within tissue samples or for use in diagnostic methods, *etc.*). Anti-AAP epitope Abs can be utilized as pharmacologically-active compounds.

- [0150]** Anti-AAP Abs can be used to isolate an AAP by standard techniques, such as immunoaffinity chromatography or immunoprecipitation. These approaches facilitate purifying an endogenous AAP antigen-containing polypeptides from 30 cells and tissues. These approaches, as well as others, can be used to detect an AAP in a sample to evaluate the abundance and pattern of expression of the antigenic protein. Anti-AAP Abs can be used to monitor protein levels in tissues as part of a clinical testing procedure; for example, to determine the efficacy of a given treatment regimen. Coupling the antibody to a detectable substance (label) allows detection of Ab-antigen complexes. Classes of labels include fluorescent, luminescent, bioluminescent, and radioactive materials, enzymes and prosthetic groups. Useful 35 labels include horseradish peroxidase, alkaline phosphatase, β -galactosidase, acetylcholinesterase, streptavidin/biotin, avidin/biotin, umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride, phycoerythrin, luminol, luciferase, luciferin, aequorin, and ¹²⁵I, ¹³¹I, ³⁵S or ³H.

11. Antibody therapeutics

- 40 **[0151]** Abs of the invention, including polyclonal, monoclonal; humanized and fully human Abs, can be used therapeutically. Such agents will generally be employed to treat or prevent a disease or pathology in a subject. An antibody preparation, preferably one having high antigen specificity and affinity generally mediates an effect by binding the target epitope(s). Generally, administration of such Abs may mediate one of two effects: (1) the antibody may prevent ligand binding, eliminating endogenous ligand binding and subsequent signal transduction, or (2) the antibody elicits a physiological result by binding an effector site on the target molecule, initiating signal transduction. 45

- [0152]** A therapeutically effective amount of an antibody relates generally to the amount needed to achieve a therapeutic objective, epitope binding affinity, administration rate, and depletion rate of the antibody from a subject. Common ranges for therapeutically effective doses may be, as a nonlimiting example, from about 0.1 mg/kg body weight to about 50 50 mg/kg body weight. Dosing frequencies may range, for example, from twice daily to once a week.

12. Pharmaceutical compositions of Abs

- 55 **[0153]** Anti-AAP Abs, as well as other AAP interacting molecules (such as aptamers) identified in other assays, can be administered in pharmaceutical compositions to treat various disorders. Principles and considerations involved in preparing such compositions, as well as guidance in the choice of components can be found in (de Boer, 1904; Gennaro, 2000; Lee, 1990).

- [0154]** Since some AAP are intracellular, Abs that are internalized are preferred used when whole Abs are used as

inhibitors. Liposomes may also be used as a delivery vehicle for intracellular introduction. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the epitope is preferred. For example, peptide molecules can be designed that bind a preferred epitope based on the variable-region sequences of a useful antibody. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology (Marasco *et al.*, 1993). Formulations may also contain more than one active compound for a particular treatment, preferably those with activities that do not adversely affect each other. The composition may comprise an agent that enhances function, such as a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent.

[0155] The active ingredients can also be entrapped in microcapsules prepared by coacervation techniques or by interfacial polymerization; for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions.

[0156] The formulations to be used for *in vivo* administration are highly preferred to be sterile. This is readily accomplished by filtration through sterile filtration membranes or any of a number of techniques.

[0157] Sustained-release preparations may also be prepared, such as semi-permeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (Boswell and Scribner, U.S. Patent No. 3,773,919, 1973), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as injectable microspheres composed of lactic acid-glycolic acid copolymer, and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods and may be preferred.

AAP recombinant expression vectors and host cells

[0158] Vectors are tools used to shuttle DNA between host cells or as a means to express a nucleotide sequence. Some vectors function only in prokaryotes, while others function in both prokaryotes and eukaryotes, enabling large-scale DNA preparation from prokaryotes for expression in eukaryotes. Inserting the DNA of interest, such as an AAP nucleotide sequence or a fragment, is accomplished by ligation techniques and/or mating protocols well-known to the skilled artisan. Such DNA is inserted such that its integration does not disrupt any necessary components of the vector. In the case of vectors that are used to express the inserted DNA protein, the introduced DNA is operably-linked to the vector elements that govern its transcription and translation.

[0159] Vectors can be divided into two general classes: Cloning vectors are replicating plasmid or phage with regions that are non-essential for propagation in an appropriate host cell, and into which foreign DNA can be inserted; the foreign DNA is replicated and propagated as if it were a component of the vector. An expression vector (such as a plasmid, yeast, or animal virus genome) is used to introduce foreign genetic material into a host cell or tissue in order to transcribe and translate the foreign DNA. In expression vectors, the introduced DNA is operably-linked to elements, such as promoters, that signal to the host cell to transcribe the inserted DNA. Some promoters are exceptionally useful, such as inducible promoters that control gene transcription in response to specific factors. Operably-linking an AAP or anti-sense construct to an inducible promoter can control the expression of an AAP or fragments, or anti-sense constructs. Examples of classic inducible promoters include those that are responsive to α -interferon, heat-shock, heavy metal ions, and steroids such as glucocorticoids (Kaufman, 1990) and tetracycline. Other desirable inducible promoters include those that are not endogenous to the cells in which the construct is being introduced, but, however, is responsive in those cells when the induction agent is exogenously supplied.

[0160] Vectors have many difference manifestations. A "plasmid" is a circular double stranded DNA molecule into which additional DNA segments can be introduced. Viral vectors can accept additional DNA segments into the viral genome. Certain vectors are capable of autonomous replication in a host cell (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. In general, useful expression vectors are often plasmids. However, other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses) are contemplated.

[0161] Recombinant expression vectors that comprise an AAP (or fragments) regulate an AAP transcription by exploiting one or more host cell-responsive (or that can be manipulated *in vitro*) regulatory sequences that is operably-linked to an AAP. "Operably-linked" indicates that a nucleotide sequence of interest is linked to regulatory sequences such that expression of the nucleotide sequence is achieved.

[0162] Vectors can be introduced in a variety of organisms and/or cells (Table D). Alternatively, the vectors can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Table D Examples of hosts for cloning or expression

Organisms	Examples	Sources and References*
Prokaryotes		
Enterobacteriaceae	<i>E. coli</i> K 12 strain MM294 X1776 W3110 K5 772	ATCC 31,446 ATCC 31,537 ATCC 27,325 ATCC 53,635
	<i>Enterobacter</i>	
	<i>Erwinia</i>	
	<i>Klebsiella</i>	
	<i>Proteus</i>	
	<i>Salmonella</i> (<i>S. typhimurium</i>)	
	<i>Serratia</i> (<i>S. marcescens</i>)	
	<i>Shigella</i>	
	<i>Bacilli</i> (<i>B. subtilis</i> and <i>B. licheniformis</i>)	
	<i>Pseudomonas</i> (<i>P. aeruginosa</i>)	
	<i>Streptomyces</i>	
Eukaryotes		
Yeasts	<i>Saccharomyces cerevisiae</i>	
	<i>Schizosaccharomyces pombe</i>	
	<i>Kluyveromyces</i> <i>K. lactis</i> MW98-8C, CBS683, CBS4574 <i>K. fragilis</i> <i>K. bulgaricus</i> <i>K. wickerhamii</i> <i>K. waltii</i> <i>K. drosophilarum</i> <i>K. thermotolerans</i> <i>K. marxianus</i> ; <i>yarrowia</i>	(Fleer <i>et al.</i> , 1991) (de Louvencourt <i>et al.</i> , 1983) ATCC 12,424 ATCC 16,045 ATCC 24,178 ATCC 56,500 ATCC 36,906 (EPO 402226, 1990)
	<i>Pichia pastoris</i>	(Sreelaishna <i>et al.</i> , 1988)
	<i>Candida</i>	
	<i>Trichoderma reesia</i>	
	<i>Neurospora crassa</i>	(Case <i>et al.</i> , 1979)
	<i>Torulopsis</i>	
	<i>Rhodotorula</i>	
	<i>Schwanniomyces</i> (<i>S. occidentalis</i>)	
	<i>Neurospora</i>	
	<i>Penicillium</i>	
Filamentous Fungi	<i>Tolypocladium</i>	(WO 91/00357, 1991)
	<i>Aspergillus</i> (<i>A. nidulans</i> and <i>A. niger</i>)	(Kelly and Hynes, 1985; Tilburn <i>et al.</i> , 1983; Yelton <i>et al.</i> , 1984)

(continued)

Organisms	Examples	Sources and References*
Invertebrate cells	<i>Drosophila</i> S2	
	<i>Spodoptera</i> Sf9	
Vertebrate cells	Chinese Hamster Ovary (CHO)	
	simian COS COS-7	ATCC CRL 1651
	HEK 293	
*Unreferenced cells are generally available from American Type Culture Collection (Manassas, VA).		

[0163] Vector choice is dictated by the organism or cells being used and the desired fate of the vector. Vectors may replicate once in the target cells, or may be "suicide" vectors. In general, vectors comprise signal sequences, origins of replication, marker genes, enhancer elements, promoters, and transcription termination sequences. The choice of these elements depends on the organisms in which the vector will be used and are easily determined. Some of these elements may be conditional, such as an inducible or conditional promoter that is turned "on" when conditions are appropriate. Examples of inducible promoters include those that are tissue-specific, which relegate expression to certain cell types, steroid-responsive, or heat-shock reactive. Some bacterial repression systems, such as the lac operon, have been exploited in mammalian cells and transgenic animals (Fieck *et al.*, 1992; Wyborski *et al.*, 1996; Wyborski and Short, 1991). Vectors often use a selectable marker to facilitate identifying those cells that have incorporated the vector. Many selectable markers are well known in the art for the use with prokaryotes, usually antibiotic-resistance genes or the use of autotrophy and auxotrophy mutants.

[0164] Using antisense and sense AAP oligonucleotides can prevent an AAP polypeptide expression. These oligonucleotides bind to target nucleic acid sequences, forming duplexes that block transcription or translation of the target sequence by enhancing degradation of the duplexes, terminating prematurely transcription or translation, or by other means.

[0165] Antisense or sense oligonucleotides are single-stranded nucleic acids, either RNA or DNA, which can bind a target AAP mRNA (sense) or an AAP DNA (antisense) sequences. According to the present invention, antisense or sense oligonucleotides comprise a fragment of an AAP DNA coding region of at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. In general, antisense RNA or DNA molecules can comprise at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 bases in length or more. Among others, (Stein and Cohen, 1988; van der Krol *et al.*, 1988a) describe methods to derive antisense or a sense oligonucleotides from a given cDNA sequence.

[0166] Modifications of antisense and sense oligonucleotides can augment their effectiveness. Modified sugar-phosphodiester bonds or other sugar linkages (WO 91/06629, 1991), increase *in vivo* stability by conferring resistance to endogenous nucleases without disrupting binding specificity to target sequences. Other modifications can increase the affinities of the oligonucleotides for their targets, such as covalently linked organic moieties (WO 90/10448, 1990) or poly-(L)-lysine. Other attachments modify binding specificities of the oligonucleotides for their targets, including metal complexes or intercalating (*e.g.* ellipticine) and alkylating agents.

[0167] To introduce antisense or sense oligonucleotides into target cells (cells containing the target nucleic acid sequence), any gene transfer method may be used and are well known to those of skill in the art. Examples of gene transfer methods include 1) biological, such as gene transfer vectors like Epstein-Barr virus or conjugating the exogenous DNA to a ligand-binding molecule (WO 91/04753, 1991), 2) physical, such as electroporation, and 3) chemical, such as CaPO₄ precipitation and oligonucleotide-lipid complexes (WO 90/10448, 1990).

[0168] The terms "host cell" and "recombinant host cell" are used interchangeably. Such terms refer not only to a particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term.

[0169] Methods of eukaryotic cell transfection and prokaryotic cell transformation are well known in the art. The choice of host cell will dictate the preferred technique for introducing the nucleic acid of interest. Table E, which is not meant to be limiting, summarizes many of the known techniques in the art. Introduction of nucleic acids into an organism may also be done with *ex vivo* techniques that use an *in vitro* method of transfection, as well as established genetic techniques, if any, for that particular organism.

Table E Methods to introduce nucleic acid into cells

Cells	Methods	References	Notes
Prokaryotes (bacteria)	Calcium chloride	(Cohen <i>et al.</i> , 1972; Hanahan, 1983; Mandel and Higa, 1970)	
	Electroporation	(Shigekawa and Dower, 1988)	
Eukaryotes	Calcium phosphate transfection	<i>N</i> -(2-Hydroxyethyl) piperazine- <i>N'</i> -(2-ethanesulfonic acid) (HEPES) buffered saline solution (Chen and Okayama, 1988; Graham and van der Eb, 1973; Wigler <i>et al.</i> , 1978)	Cells may be "shocked" with glycerol or dimethylsulfoxide (DMSO) to increase transfection efficiency (Ausubel <i>et al.</i> , 1987).
Mammalian cells		BES (<i>N,N</i> -bis(2-hydroxyethyl)-2-aminoethanesulfonic acid) buffered solution (Ishiura <i>et al.</i> , 1982)	
	Diethylaminoethyl (DEAE)-Dextran transfection	(Fujita <i>et al.</i> , 1986; Lopata <i>et al.</i> , 1984; Selden <i>et al.</i> , 1986)	Most useful for transient, but not stable, transfections. Chloroquine can be used to increase efficiency.
	Electroporation	(Neumann <i>et al.</i> , 1982; Potter, 1988; Potter <i>et al.</i> , 1984; Wong and Neumann, 1982)	Especially useful for hard-to-transfect lymphocytes.
	Cationic lipid reagent transfection	(Elroy-Stein and Moss, 1990; Felgner <i>et al.</i> , 1987; Rose <i>et al.</i> , 1991; Whitt <i>et al.</i> , 1990)	Applicable to both <i>in vivo</i> and <i>in vitro</i> transfection.
	Retroviral	Production exemplified by (Cepko <i>et al.</i> , 1984; Miller and Buttimore, 1986; Pear <i>et al.</i> , 1993) Infection <i>in vitro</i> and <i>in vivo</i> : (Austin and Cepko, 1990; Bodine <i>et al.</i> , 1991; Fekete and Cepko, 1993; Lemischka <i>et al.</i> , 1986; Turner <i>et al.</i> , 1990; Williams <i>et al.</i> , 1984)	Lengthy process, many packaging lines available at ATCC. Applicable to both <i>in vivo</i> and <i>in vitro</i> transfection.
	Polybrene	(Chaney <i>et al.</i> , 1986; Kawai and Nishizawa, 1984)	
	Microinjection	(Capecchi, 1980)	Can be used to establish cell lines carrying integrated copies of AAP DNA sequences.

(continued)

Cells	Methods	References	Notes
	Protoplast fusion	(Rassoulzadegan <i>et al.</i> , 1982; Sandri-Goldin <i>et al.</i> , 1981; Schaffner, 1980)	
Insect cells (<i>in vitro</i>)	Baculovirus systems	(Luckow, 1991; Miller, 1988; O'Reilly <i>et al.</i> , 1992)	Useful for <i>in vitro</i> production of proteins with eukaryotic modifications.
Yeast	Electroporation	(Becker and Guarente, 1991)	
	Lithium acetate	(Gietz <i>et al.</i> , 1998; Ito <i>et al.</i> , 1983)	
	Spheroplast fusion	(Beggs, 1978; Hinnen <i>et al.</i> , 1978)	Laborious, can produce aneuploids.
Plant cells (general reference: (Hansen and Wright, 1999))	Agrobacterium transformation	(Bechtold and Pelletier, 1998; Escudero and Hohn, 1997; Hansen and Chilton, 1999; Touraev and al., 1997)	
	Biolistics (microprojectiles)	(Finer <i>et al.</i> , 1999; Hansen and Chilton, 1999; Shillito, 1999)	
	Electroporation (protoplasts)	(Fromm <i>et al.</i> , 1985; Ou-Lee <i>et al.</i> , 1986; Rhodes <i>et al.</i> , 1988; Saunders <i>et al.</i> , 1989) May be combined with liposomes (Trick and al., 1997)	
	Polyethylene glycol (PEG) treatment	(Shillito, 1999)	
	Liposomes	May be combined with electroporation (Trick and al., 1997)	
	<i>in planta</i> microinjection	(Leduc and al., 1996; Zhou and al., 1983)	
	Seed imbibition	(Trick and al., 1997)	
	Laser beam	(Hoffman, 1996)	
	Silicon carbide whiskers	(Thompson and al., 1995)	

[0170] Vectors often use a selectable marker to facilitate identifying those cells that have incorporated the vector. Many selectable markers are well known in the art for the use with prokaryotes, usually antibiotic-resistance genes or the use of autotrophy and auxotrophy mutants. Table F lists often-used selectable markers for mammalian cell transfection.

Table F Useful selectable markers for eukaryote cell transfection

Selectable Marker	Selection	Action	Reference
Adenosine deaminase (ADA)	Media includes 9- β -D-xylofuranosyl adenine (Xyl-A)	Conversion of Xyl-A to Xyl-ATP, which incorporates into nucleic acids, killing cells. ADA detoxifies	(Kaufman <i>et al.</i> , 1986)
Dihydrofolate reductase (DHFR)	Methotrexate(MTX) and dialyzed serum (purine-free media)	MTX competitive inhibitor of DHFR. In absence of exogenous purines, cells require DHFR, a necessary enzyme in purine biosynthesis.	(Simonsen and Levinson, 1983)
Aminoglycoside phosphotransferase ("APH", "neo", "G418")	G418	G418, an aminoglycoside detoxified by APH, interferes with ribosomal function and consequently, translation.	(Southern and Berg, 1982)
Hygromycin-B-phosphotransferase (HPH)	hygromycin-B	Hygromycin-B, an aminocyclitol detoxified by HPH, disrupts protein translocation and promotes mistranslation.	(Palmer <i>et al.</i> , 1987)
Thymidine kinase (TK)	Forward selection (TK+): Media (HAT) incorporates aminopterin. Reverse selection (TK-): Media incorporates 5-bromodeoxyuridine (BrdU).	Forward: Aminopterin forces cells to synthesize dTTP from thymidine, a pathway requiring TK. Reverse: TK phosphorylates BrdU, which incorporates into nucleic acids, killing cells.	(Littlefield, 1964)

[0171] A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce an AAP. Accordingly, the invention provides methods for producing an AAP using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of the invention (into which a recombinant expression vector encoding an AAP has been introduced) in a suitable medium, such that an AAP is produced. In another embodiment, the method further comprises isolating an AAP from the medium or the host cell.

Transgenic AAP animals

[0172] Transgenic animals are useful for studying the function and/or activity of an AAP and for identifying and/or evaluating modulators of AAP activity. "Transgenic animals" are non-human animals, preferably mammals, more preferably a rodents such as rats or mice, in which one or more of the cells include a transgene. Other transgenic animals include primates, sheep; dogs, cows, goats, chickens, amphibians, *etc.* A "transgene" is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops, and that remains in the genome of the mature animal. Transgenes preferably direct the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal with the purpose of preventing expression of a naturally encoded gene product in one or more cell types or tissues (a "knockout" transgenic animal), or serving as a marker or indicator of an integration, chromosomal location, or region of recombination (*e.g. cre/loxP* mice). A "homologous recombinant animal" is a non-human animal, such as a rodent, in which an endogenous AAP has been altered by an exogenous DNA molecule that recombines homologously with an endogenous AAP in a (*e.g. embryonic*) cell prior to development the animal. Host cells with an exogenous AAP can be used to produce non-human transgenic animals, such as fertilized oocytes or embryonic stem cells into which an AAP-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals or homologous recombinant animals.

1. Approaches to transgenic animal production

[0173] A transgenic animal can be created by introducing an *AAP* into the male pronuclei of a fertilized oocyte (*e.g.*, by microinjection, retroviral infection) and allowing the oocyte to develop in a pseudopregnant female foster animal (*pffa*). An *AAP* cDNA sequences (SEQ ID NO: 3) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a homologue of an *AAP*, such as the naturally-occurring variant of an *AAP*, can be used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase transgene expression. Tissue-specific regulatory sequences can be operably-linked to the *AAP* transgene to direct expression of the *AAP* to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art, *e.g.* (Evans *et al.*, U.S. Patent No. 4,870,009, 1989; Hogan, 0879693843, 1994; Leder and Stewart, U.S. Patent No. 4,736,866, 1988; Wagner and Hoppe, US Patent No. 4,873,191, 1989). Other non-mice transgenic animals may be made by similar methods. A transgenic founder animal, which can be used to breed additional transgenic animals, can be identified based upon the presence of the transgene in its genome and/or expression of the transgene mRNA in tissues or cells of the animals. Transgenic animals can be bred to other transgenic animals carrying other transgenes.

2. Vectors for transgenic animal production

[0174] To create a homologous recombinant animal, a vector containing at least a portion of an *AAP* into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, disrupt or alter the expression of, an *AAP*. An *AAP* can be a murine gene, or other *AAP* homologue, such as a naturally occurring variant. In one approach, a knockout vector functionally disrupts an endogenous *AAP* gene upon homologous recombination, and thus a non-functional *AAP* protein, if any, is expressed.

[0175] Alternatively, the vector can be designed such that, upon homologous recombination, an endogenous *AAP* is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of an endogenous *AAP*). In this type of homologous recombination vector, the altered portion of the *AAP* is flanked at its 5'- and 3'-termini by additional nucleic acid of the *AAP* to allow for homologous recombination to occur between the exogenous *AAP* carried by the vector and an endogenous *AAP* in an embryonic stem cell. The additional flanking *AAP* nucleic acid is sufficient to engender homologous recombination with the endogenous *AAP*. Typically, several kilobases of flanking DNA (both at the 5'- and 3'-termini) are included in the vector (Thomas and Capecchi, 1987). The vector is then introduced into an embryonic stem cell line (*e.g.*, by electroporation), and cells in which the introduced *AAP* has homologously-recombined with an endogenous *AAP* are selected (Li *et al.*, 1992).

3. Introduction of an *AAP* transgene cells during development

[0176] Selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras (Bradley, 1987). A chimeric embryo can then be implanted into a suitable *pffa* and the embryo brought to term. Progeny harboring the homologously-recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously-recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described (Berns *et al.*, WO 93/04169, 1993; Bradley, 1991; Kucherlapati *et al.*, WO 91/01140, 1991; Le Mouellic and Brullet, WO 90/11354, 1990).

[0177] Alternatively, transgenic animals that contain selected systems that allow for regulated expression of the transgene can be produced. An example of such a system is the *cre/loxP* recombinase system of bacteriophage P1 (Lakso *et al.*, 1992). Another recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.*, 1991). If a *cre/loxP* recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the *Cre* recombinase and a selected protein are required. Such animals can be produced as "double" transgenic animals, by mating an animal containing a transgene encoding a selected protein to another containing a transgene encoding a recombinase.

[0178] Clones of transgenic animals can also be produced (Wilmot *et al.*, 1997). In brief, a cell from a transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured to develop to a morula or blastocyte and then transferred to a *pffa*. The offspring borne of this female foster animal will be a clone of the "parent" transgenic animal.

Pharmaceutical compositions

[0179] The *AAP* nucleic acid molecules, *AAP* polypeptides, and anti-*AAP* Abs (active compounds) of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions. Such

compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. A "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration (Gennaro, 2000). Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. Except when a conventional media or agent is incompatible with an active compound, use of these compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

1. General considerations

[0180] A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration, including intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (*i.e.*, topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

2. Injectable formulations

[0181] Pharmaceutical compositions suitable for injection include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, CREMOPHOR EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid so as to be administered using a syringe. Such compositions should be stable during manufacture and storage and must be preserved against contamination from microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (such as glycerol, propylene glycol, and liquid polyethylene glycol), and suitable mixtures. Proper fluidity can be maintained, for example, by using a coating such as lecithin, by maintaining the required particle size in the case of dispersion and by using surfactants. Various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, and thimerosal, can contain microorganism contamination. Isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, and sodium chloride can be included in the composition. Compositions that can delay absorption include agents such as aluminum monostearate and gelatin.

[0182] Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, an AAP or anti-AAP antibody) in the required amount in an appropriate solvent with one or a combination of ingredients as required, followed by sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium, and the other required ingredients as discussed. Sterile powders for the preparation of sterile injectable solutions, methods of preparation include vacuum drying and freeze-drying that yield a powder containing the active ingredient and any desired ingredient from a sterile solutions.

3. Oral compositions

[0183] Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included. Tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, PRIMOGEL, or corn starch; a lubricant such as magnesium stearate or STEROTES; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

4. Compositions for inhalation

[0184] For administration by inhalation, the compounds are delivered as an aerosol spray from a nebulizer or a

pressurized container that contains a suitable propellant, *e.g.*, a gas such as carbon dioxide.

5. Systemic administration

[0185] Systemic administration can also be transmucosal or transdermal. For transmucosal or transdermal administration, penetrants that can permeate the target barrier(s) are selected. Transmucosal penetrants include, detergents, bile salts, and fusidic acid derivatives. Nasal sprays or suppositories can be used for transmucosal administration. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams.

[0186] The compounds can also be prepared in the form of suppositories (*e.g.*, with bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

6. Carriers

[0187] In one embodiment, the active compounds are prepared with carriers that protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Such materials can be obtained commercially from ALZA Corporation (Mountain View, CA) and NOVA Pharmaceuticals, Inc. (Lake Elsinore, CA), or prepared by one of skill in the art. Liposomal suspensions can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, such as in (Eppstein *et al.*, US Patent No. 4,522,811, 1985),

7. Unit dosage.

[0188] Oral formulations or parenteral compositions in unit dosage form can be created to facilitate administration and dosage uniformity. Unit dosage form refers to physically discrete units suited as single dosages for the subject to be treated, containing a therapeutically effective quantity of active compound in association with the required pharmaceutical carrier. The specification for the unit dosage forms of the invention are dictated by, and directly dependent on, the unique characteristics of the active compound and the particular desired therapeutic effect, and the inherent limitations of compounding the active compound.

8. Gene therapy compositions

[0189] The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (Nabel and Nabel, US Patent No. 5,328,470, 1994), or by stereotactic injection (Chen *et al.*, 1994). The pharmaceutical preparation of a gene therapy vector can include an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

9. Dosage

[0190] The pharmaceutical composition and method of the present invention may further comprise other therapeutically active compounds as noted herein that are usually applied in the treatment of the above mentioned pathological conditions.

[0191] In the treatment or prevention of conditions which require AAP modulation an appropriate dosage level will generally be about 0.01 to 500 mg per kg patient body weight per day which can be administered in single or multiple doses. Preferably, the dosage level will be about 0.1 to about 250 mg/kg per day; more preferably about 0.5 to about 100 mg/kg per day. A suitable dosage level may be about 0.01 to 250 mg/kg per day, about 0.05 to 100 mg/kg per day, or about 0.1 to 50 mg/kg per day. Within this range the dosage may be 0.05 to 0.5, 0.5 to 5 or 5 to 50 mg/kg per day. For oral administration, the compositions are preferably provided in the form of tablets containing 1.0 to 1000 milligrams of the active ingredient, particularly 1.0, 5.0, 10.0, 15.0, 20.0, 25.0, 50.0, 75.0, 100.0, 150.0, 200.0, 250.0, 300.0, 400.0, 500.0, 600.0, 750.0, 800.0, 900.0, and 1000.0 milligrams of the active ingredient for the symptomatic adjustment of the dosage to the patient to be treated. The compounds may be administered on a regimen of 1 to 4 times per day, preferably once or twice per day.

[0192] It will be understood, however, that the specific dose level and frequency of dosage for any particular patient may be varied and will depend upon a variety of factors including the activity of the specific compound employed, the metabolic stability and length of action of that compound, the age, body weight, general health, sex, diet, mode and time

of administration, rate of excretion, drug combination, the severity of the particular condition, and the host undergoing therapy.

10. Kits for pharmaceutical compositions

[0193] The pharmaceutical compositions can be included in a kit, container, pack, or dispenser together with instructions for administration. When the invention is supplied as a kit, the different components of the composition may be packaged in separate containers and admixed immediately before use. Such packaging of the components separately may permit long-term storage without losing the active components' functions.

[0194] Kits may also include reagents in separate containers that facilitate the execution of a specific test, such as diagnostic tests or tissue typing. For example, AAP DNA templates and suitable primers may be supplied for internal controls.

(a) Containers or vessels

[0195] The reagents included in the kits can be supplied in containers of any sort such that the life of the different components are preserved, and are not adsorbed or altered by the materials of the container. For example, sealed glass ampules may contain lyophilized luciferase or buffer that have been packaged under a neutral, non-reacting gas, such as nitrogen. Ampoules may consist of any suitable material, such as glass, organic polymers, such as polycarbonate, polystyrene, etc., ceramic, metal or any other material typically employed to hold reagents. Other examples of suitable containers include simple bottles that may be fabricated from similar substances as ampules, and envelopes, that may consist of foil-lined interiors, such as aluminum or an alloy. Other containers include test tubes, vials, flasks, bottles, syringes, or the like. Containers may have a sterile access port, such as a bottle having a stopper that can be pierced by a hypodermic injection needle. Other containers may have two compartments that are separated by a readily removable membrane that upon removal permits the components to mix. Removable membranes may be glass, plastic, rubber, etc.

(b) Instructional materials

[0196] Kits may also be supplied with instructional materials. Instructions may be printed on paper or other substrate, and/or may be supplied as an electronic-readable medium, such as a floppy disc, CD-ROM, DVD-ROM, Zip disc, videotape, audiotape, etc. Detailed instructions may not be physically associated with the kit; instead, a user may be directed to an internet web site specified by the manufacturer or distributor of the kit, or supplied as electronic mail.

Screening and detection methods

[0197] The isolated nucleic acid molecules of the invention can be used to express an AAP (e.g., via a recombinant expression vector in a host cell in gene therapy applications), to detect an AAP mRNA (e.g., in a biological sample) or a genetic lesion in an AAP, and to modulate AAP activity, as described below. In addition, AAP polypeptides can be used to screen drugs or compounds that modulate the AAP activity or expression as well as to treat disorders characterized by insufficient or excessive production of an AAP or production of AAP forms that have decreased or aberrant activity compared to an AAP wild-type protein, or modulate biological function that involve an AAP. In addition, the anti-AAP Abs of the invention can be used to detect and isolate an AAP and modulate AAP activity.

1. Screening assays

[0198] The invention provides a method (screening assay) for identifying modalities, i.e., candidate or test compounds or agents (e.g., peptides, peptidomimetics, small molecules or other drugs), foods, combinations thereof, etc., that effect an AAP, a stimulatory or inhibitory effect, including translation, transcription, activity or copies of the gene in cells. The invention also includes compounds identified in screening assays.

[0199] Testing for compounds that increase or decrease AAP activity are desirable. A compound may modulate an AAP activity by affecting: (1) the number of copies of the gene in the cell (amplifiers and deamplifiers); (2) increasing or decreasing transcription of an AAP (transcription up-regulators and down-regulators); (3) by increasing or decreasing the translation of an AAP mRNA into protein (translation up-regulators and down-regulators); or (4) by increasing or decreasing the activity of an AAP itself (agonists and antagonists).

(a) effects of compounds

[0200] To identify compounds that affect an AAP at the DNA, RNA and protein levels, cells or organisms are contacted

with a candidate compound and the corresponding change in an AAP DNA, RNA or protein is assessed (Ausubel *et al.*, 1987). For DNA amplifiers and deamplifiers, the amount of an AAP DNA is measured, for those compounds that are transcription up-regulators and down-regulators the amount of an AAP mRNA is determined; for translational up- and down-regulators, the amount of an AAP polypeptide is measured. Compounds that are agonists or antagonists may be identified by contacting cells or organisms with the compound, and then examining, for example, the model of angiogenesis *in vitro*.

[0201] In one embodiment, many assays for screening candidate or test compounds that bind to or modulate the activity of an AAP or polypeptide or biologically-active portion are available. Test compounds can be obtained using any of the numerous approaches in combinatorial library methods, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptides, while the other four approaches encompass peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997).

(b) *small molecules*

[0202] A "small molecule" refers to a composition that has a molecular weight of less than about 5 kD and more preferably less than about 4 kD, most preferably less than 0.6 kD. Small molecules can be, nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened with any of the assays of the invention. Examples of methods for the synthesis of molecular libraries can be found in: (Carell *et al.*, 1994a; Carell *et al.*, 1994b; Cho *et al.*, 1993; DeWitt *et al.*, 1993; Gallop *et al.*, 1994; Zuckermann *et al.*, 1994).

[0203] Libraries of compounds may be presented in solution (Houghten *et al.*, 1992) or on beads (Lam *et al.*, 1991), on chips (Fodor *et al.*, 1993), bacteria, spores (Ladner *et al.*, US Patent No. 5,223,409, 1993), plasmids (Cull *et al.*, 1992) or on phage (Cwirla *et al.*, 1990; Devlin *et al.*, 1990; Felici *et al.*, 1991; Ladner *et al.*, US Patent No. 5,223,409, 1993; Scott and Smith, 1990). A cell-free assay comprises contacting an AAP or biologically-active fragment with a known compound that binds the AAP to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with the AAP, where determining the ability of the test compound to interact with the AAP comprises determining the ability of the AAP to preferentially bind to or modulate the activity of an AAP target molecule.

(c) *cell-free assays*

[0204] The cell-free assays of the invention may be used with both soluble or a membrane-bound forms of an AAP. In the case of cell-free assays comprising the membrane-bound form, a solubilizing agent to maintain the AAP in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, TRITON® X-100 and others from the TRITON® series, THESIT®, Isotridecypoly(ethylene glycol ether)_n, N-dodecyl-N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl) dimethylamminiol-1-propane sulfonate (CHAPS); or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

(d) *immobilization of target molecules to facilitate screening*

[0205] In more than one embodiment of the assay methods, immobilizing either an AAP or its partner molecules can facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate high throughput assays. Binding of a test compound to an AAP, or interaction of an AAP with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants, such as microtiter plates, test tubes, and micro-centrifuge tubes. A fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, GST-AAP fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (SIGMA Chemical, St. Louis, MO) or glutathione derivatized microtiter plates that are then combined with the test compound or the test compound and either the non-adsorbed target protein or an AAP, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described. Alternatively, the complexes can be dissociated from the matrix, and the level of AAP binding or activity determined using standard techniques.

[0206] Other techniques for immobilizing proteins on matrices can also be used in screening assays. Either an AAP or its target molecule can be immobilized using biotin-avidin or biotin-streptavidin systems. Biotinylation can be accom-

plished using many reagents, such as biotin-NHS (N-hydroxy-succinimide; PIERCE Chemicals, Rockford, IL), and immobilized in wells of streptavidin-coated 96 well plates (PIERCE Chemical). Alternatively, Abs reactive with an AAP or target molecules, but which do not interfere with binding of the AAP to its target molecule, can be derivatized to the wells of the plate, and unbound target or an AAP trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described for the GST-immobilized complexes, include immunodetection of complexes using Abs reactive with an AAP or its target, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the AAP or target molecule.

(e) *screens to identify modulators*

[0207] Modulators of AAP expression can be identified in a method where a cell is contacted with a candidate compound and the expression of an AAP mRNA or protein in the cell is determined. The expression level of the AAP mRNA or protein in the presence of the candidate compound is compared to the AAP mRNA or protein levels in the absence of the candidate compound. The candidate compound can then be identified as a modulator of the AAP mRNA or protein expression based upon this comparison. For example, when expression of an AAP mRNA or protein is greater (*i.e.*, statistically significant) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of the AAP mRNA or protein expression. Alternatively, when expression of the AAP mRNA or protein is less (statistically significant) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of the AAP mRNA or protein expression. The level of an AAP mRNA or protein expression in the cells can be determined by methods described for detecting an AAP mRNA or protein.

(i) *hybrid assays*

[0208] In yet another aspect of the invention, an AAP can be used as "bait" in two-hybrid or three hybrid assays (Bartel *et al.*, 1993; Brent *et al.*, WO94/10300, 1994; Iwabuchi *et al.*, 1993; Madura *et al.*, 1993; Saifer *et al.*, US Patent No. 5,283,317, 1994; Zervos *et al.*, 1993) to identify other proteins that bind or interact with the AAP and modulate AAP activity. Such AAP-bps are also likely to be involved in the propagation of signals by the AAP as, for example, upstream or downstream elements of an AAP pathway.

[0209] The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for an AAP is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL4). The other construct, a DNA sequence from a library of DNA sequences that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact *in vivo*, forming an AAP-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably-linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected, and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the AAP-interacting protein.

[0210] The invention further pertains to novel agents identified by the aforementioned screening assays and uses thereof for treatments as described herein.

2. *Detection assays*

[0211] Portions or fragments of an AAP cDNA sequences identified herein (and the complete AAP gene sequences) are useful in themselves. By way of non-limiting example, these sequences can be used to: (1) identify an individual from a minute biological sample (tissue typing); and (2) aid in forensic identification of a biological sample.

(a) *Tissue typing*

[0212] The AAP sequences of the invention can be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes and probed on a Southern blot to yield unique bands. The sequences of the invention are useful as additional DNA markers for "restriction fragment length polymorphisms" (RFLP; (Smulson *et al.*, US Patent No. 5,272,057, 1993)).

[0213] Furthermore, the AAP sequences can be used to determine the actual base-by-base DNA sequence of targeted portions of an individual's genome. AAP sequences can be used to prepare two PCR primers from the 5'- and 3'-termini of the sequences that can then be used to amplify an the corresponding sequences from an individual's genome and then sequence the amplified fragment

[0214] Panels of corresponding DNA sequences from individuals can provide unique individual identifications, as each

individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the invention can be used to obtain such identification sequences from individuals and from tissue. The AAP sequences of the invention uniquely represent portions of an individual's genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. The allelic variation between individual humans occurs with a frequency of about once every 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include RFLPs.

[0215] Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in noncoding regions, fewer sequences are necessary to differentiate individuals. Noncoding sequences can positively identify individuals with a panel of 10 to 1,400 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences, such as SEQ ID NO: 3 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive medicine

[0216] The invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to treat an individual prophylactically. Accordingly, one aspect of the invention relates to diagnostic assays for determining an AAP and/or nucleic acid expression as well as AAP activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant AAP expression or activity, including cancer. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with an AAP, nucleic acid expression or activity. For example, mutations in an AAP can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to prophylactically treat an individual prior to the onset of a disorder characterized by or associated with the AAP, nucleic acid expression, or biological activity.

[0217] Another aspect of the invention provides methods for determining AAP activity, or nucleic acid expression, in an individual to select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of modalities (*e.g.*, drugs, foods) for therapeutic or prophylactic treatment of an individual based on the individual's genotype (*e.g.*, the individual's genotype to determine the individual's ability to respond to a particular agent). Another aspect of the invention pertains to monitoring the influence of modalities (*e.g.*, drugs, foods) on the expression or activity of an AAP in clinical trials.

1. Diagnostic assays

[0218] An exemplary method for detecting the presence or absence of an AAP in a biological sample involves obtaining a biological sample from a subject and contacting the biological sample with a compound or an agent capable of detecting the AAP or the AAP nucleic acid (*e.g.*, mRNA, genomic DNA) such that the presence of the AAP is confirmed in the sample. An agent for detecting the AAP mRNA or genomic DNA is a labeled nucleic acid probe that can hybridize to the AAP mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length AAP nucleic acid, such as the nucleic acid of SEQ ID NO:3, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to an AAP mRNA or genomic DNA.

[0219] An agent for detecting an AAP polypeptide is an antibody capable of binding to the AAP, preferably an antibody with a detectable label. Abs can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment (*e.g.*, F_{ab} or F(ab')₂) can be used. A labeled probe or antibody is coupled (*i.e.*, physically linking) to a detectable substance, as well as indirect detection of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" includes tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. The detection method of the invention can be used to detect an AAP mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of an AAP mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of an AAP polypeptide include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of an AAP genomic DNA include Southern hybridizations and fluorescence *in situ* hybridization (FISH). Furthermore, *in vivo* techniques for detecting an AAP include introducing into a subject a labeled anti-AAP antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

[0220] In one embodiment, the biological sample from the subject contains protein molecules, and/or mRNA molecules, and/or genomic DNA molecules. A preferred biological sample is blood.

[0221] In another embodiment, the methods further involve obtaining a biological sample from a subject to provide a control, contacting the sample with a compound or agent to detect an AAP, mRNA, or genomic DNA, and comparing the presence of the AAP, mRNA or genomic DNA in the control sample with the presence of the AAP, mRNA or genomic DNA in the test sample.

[0222] The invention also encompasses kits for detecting an AAP in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting an AAP or an AAP mRNA in a sample; reagent and/or equipment for determining the amount of an AAP in the sample; and reagent and/or equipment for comparing the amount of an AAP in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect the AAP or nucleic acid.

2. Prognostic assays

[0223] The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with an aberrant AAP expression or activity. For example, the assays described herein, can be used to identify a subject having or at risk of developing a disorder associated with AAP, nucleic acid expression or activity. Alternatively, the prognostic assays can be used to identify a subject having or at risk for developing a disease or disorder. The invention provides a method for identifying a disease or disorder associated with an aberrant AAP expression or activity in which a test sample is obtained from a subject and the AAP or nucleic acid (e.g., mRNA, genomic DNA) is detected. A test sample is a biological sample obtained from a subject. For example, a test sample can be a biological fluid (e.g., serum), cell sample, or tissue.

[0224] Prognostic assays can be used to determine whether a subject can be administered a modality (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, food, etc.) to treat a disease or disorder associated with an aberrant AAP expression or activity. Such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder. The invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with an aberrant AAP expression or activity in which a test sample is obtained and the AAP or nucleic acid is detected (e.g., where the presence of the AAP or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with the aberrant AAP expression or activity).

[0225] The methods of the invention can also be used to detect genetic lesions in an AAP to determine if a subject with the genetic lesion is at risk for a disorder characterized by aberrant angiogenesis. Methods include detecting, in a sample from the subject, the presence or absence of a genetic lesion characterized by at an alteration affecting the integrity of a gene encoding an AAP polypeptide, or the mis-expression of an AAP. Such genetic lesions can be detected by ascertaining: (1) a deletion of one or more nucleotides from an AAP; (2) an addition of one or more nucleotides to an AAP; (3) a substitution of one or more nucleotides in an AAP, (4) a chromosomal rearrangement of an AAP gene; (5) an alteration in the level of an AAP mRNA transcripts, (6) aberrant modification of an AAP, such as a change genomic DNA methylation, (7) the presence of a non-wild-type splicing pattern of an AAP mRNA transcript, (8) a non-wild-type level of an AAP, (9) allelic loss of an AAP, and/or (10) inappropriate post-translational modification of an AAP polypeptide. There are a large number of known assay techniques that can be used to detect lesions in an AAP. Any biological sample containing nucleated cells may be used.

[0226] In certain embodiments, lesion detection may use a probe/primer in a polymerase chain reaction (PCR) (e.g., Mullis, US Patent No. 4,683,202, 1987; Mullis *et al.*, US Patent No. 4,683,195, 1987), such as anchor PCR or rapid amplification of cDNA ends (RACE) PCR, or, alternatively, in a ligation chain reaction (LCR) (e.g., Landegren *et al.*, 1988; Nakazawa *et al.*, 1994), the latter is particularly useful for detecting point mutations in AAP-genes (Abravaya *et al.*, 1995). This method may include collecting a sample from a patient, isolating nucleic acids from the sample, contacting the nucleic acids with one or more primers that specifically hybridize to an AAP under conditions such that hybridization and amplification of the AAP (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

[0227] Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990), transcriptional amplification system (Kwoh *et al.*, 1989); Q β Replicase (Lizardi *et al.*, 1988), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules present in low abundance.

[0228] Mutations in an AAP from a sample can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

[0229] Hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high-density arrays containing hundreds or thousands of oligonucleotides probes, can identify genetic mutations in an AAP (Cronin *et al.*, 1996; Kozal *et al.*, 1996). For example, genetic mutations in an AAP can be identified in two-dimensional arrays containing light-generated DNA probes as described in Cronin, *et al.*, *supra*. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

[0230] In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence an AAP and detect mutations by comparing the sequence of the sample AAP-with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on classic techniques (Maxam and Gilbert, 1977; Sanger *et al.*, 1977). Any of a variety of automated sequencing procedures can be used when performing diagnostic assays (Naeve *et al.*, 1995) including sequencing by mass spectrometry (Cohen *et al.*, 1996; Griffin and Griffin, 1993; Koster, WO94/16101, 1994).

[0231] Other methods for detecting mutations in an AAP include those in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes (Myers *et al.*, 1985). In general, the technique of "mismatch cleavage" starts by providing heteroduplexes formed by hybridizing (labeled) RNA or DNA containing a wild-type AAP sequence with potentially mutant RNA or DNA obtained from a sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as those that arise from base pair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S₁ nuclease to enzymatically digest the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. The digested material is then separated by size on denaturing polyacrylamide gels to determine the mutation site (Grompe *et al.*, 1989; Saleeba and Cotton, 1993). The control DNA or RNA can be labeled for detection.

[0232] Mismatch cleavage reactions may employ one or more proteins that recognize mismatched base pairs in double-stranded DNA (DNA mismatch repair) in defined systems for detecting and mapping point mutations in an AAP cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu *et al.*, 1994). According to an exemplary embodiment, a probe based on a wild-type AAP sequence is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like (Modrich *et al.*, US Patent No. 5,459,039, 1995).

[0233] Electrophoretic mobility alterations can be used to identify mutations in an AAP. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Cotton, 1993; Hayashi, 1992; Orita *et al.*, 1989). Single-stranded DNA fragments of sample and control AAP nucleic acids are denatured and then renatured. The secondary structure of single-stranded nucleic acids varies according to sequence; the resulting alteration in electrophoretic mobility allows detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a sequence changes. The subject method may use heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen *et al.*, 1991).

[0234] The migration of mutant or wild-type fragments can be assayed using denaturing gradient gel electrophoresis (DGGE; (Myers *et al.*, 1985). In DGGE, DNA is modified to prevent complete denaturation, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. A temperature gradient may also be used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA (Rossiter and Caskey, 1990).

[0235] Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found (Saiki *et al.*, 1986; Saiki *et al.*, 1989). Such allele-specific oligonucleotides are hybridized to PCR-amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

[0236] Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used. Oligonucleotide primers for specific amplifications may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization (Gibbs *et al.*, 1989)) or at the extreme 3'-terminus of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prosser, 1993). Novel restriction site in the region of the mutation may be introduced to create cleavage-based detection (Gasparini *et al.*, 1992). Certain amplification may also be performed using *Taq* ligase for amplification (Barany, 1991). In such cases,

ligation occurs only if there is a perfect match at the 3'-terminus of the 5' sequence, allowing detection of a known mutation by scoring for amplification.

[0237] The described methods may be performed, for example, by using pre-packaged kits comprising at least one probe (nucleic acid or antibody) that may be conveniently used, for example, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving an AAP.

[0238] Furthermore, any cell type or tissue in which an AAP is expressed may be utilized in the prognostic assays described herein.

3. Pharmacogenomics

[0239] Agents, or modulators that have a stimulatory or inhibitory effect on AAP activity or expression, as identified by a screening assay can be administered to individuals to treat, prophylactically or therapeutically, disorders, including those associated with angiogenesis. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between a subject's genotype and the subject's response to a foreign modality, such as a food, compound or drug) may be considered. Metabolic differences of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of an AAP, expression of an AAP nucleic acid, or an AAP mutation(s) in an individual can be determined to guide the selection of appropriate agent(s) for therapeutic or prophylactic treatment.

[0240] Pharmacogenomics deals with clinically significant hereditary variations in the response to modalities due to altered modality disposition and abnormal action in affected persons (Eichelbaum and Evert, 1996; Linder *et al.*, 1997). In general, two pharmacogenetic conditions can be differentiated: (1) genetic conditions transmitted as a single factor altering the interaction of a modality with the body (altered drug action) or (2) genetic conditions transmitted as single factors altering the way the body acts on a modality (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as nucleic acid polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

[0241] As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) explains the phenomena of some patients who show exaggerated drug response and/or serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the *CYP2D6* gene is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers due to mutant *CYP2D6* and *CYP2C19* frequently experience exaggerated drug responses and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM shows no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so-called ultra-rapid metabolizers who are unresponsive to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

[0242] The activity of an AAP, expression of an AAP nucleic acid, or mutation content of an AAP in an individual can be determined to select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an AAP modulator, such as a modulator identified by one of the described exemplary screening assays.

4. Monitoring effects during clinical trials

[0243] Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of an AAP (*e.g.*, the ability to modulate angiogenesis) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent determined by a screening assay to increase an AAP expression, protein levels, or up-regulate an AAP's activity can be monitored in clinical trials of subjects exhibiting decreased AAP expression, protein levels, or down-regulated AAP activity. Alternatively, the effectiveness of an agent determined to decrease an AAP expression, protein levels, or down-regulate an AAP's activity, can be monitored in clinical trials of subjects exhibiting increased the AAP expression, protein levels, or up-regulated AAP activity. In such clinical trials, the expression or

activity of the AAP and, preferably, other genes that have been implicated in, for example, angiogenesis can be used as a "read out" or markers for a particular cell's responsiveness.

[0244] For example, genes, including an AAP, that are modulated in cells by treatment with a modality (e.g., food, compound, drug or small molecule) can be identified. To study the effect of agents on angiogenesis, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of an AAP and other genes implicated in the disorder. The gene expression pattern can be quantified by Northern blot analysis, nuclear run-on or RT-PCR experiments, or by measuring the amount of protein, or by measuring the activity level of the AAP or other gene products. In this manner, the gene expression pattern itself can serve as a marker, indicative of the cellular physiological response to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

[0245] The invention provides but does not claim a method for monitoring the effectiveness of treatment of a subject with an agent (e.g., an agonist, antagonist, protein, peptide, peptidomimetic, nucleic acid, small molecule, food or other drug candidate identified by the screening assays described herein) comprising the steps of (1) obtaining a pre-administration sample from a subject; (2) detecting the level of expression of an AAP, mRNA, or genomic DNA in the pre-administration sample; (3) obtaining one or more post-administration samples from the subject; (4) detecting the level of expression or activity of the AAP, mRNA, or genomic DNA in the post-administration samples; (5) comparing the level of expression or activity of the AAP, mRNA, or genomic DNA in the pre-administration sample with the AAP, mRNA, or genomic DNA in the post administration sample or samples; and (6) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of the AAP to higher levels than detected, i.e., to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of the AAP to lower levels than detected, i.e., to decrease the effectiveness of the agent.

5. Methods of treatment

[0246] The invention provides but does not claim for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant AAP expression or activity. Furthermore, these same methods of treatment may be used to induce or inhibit angiogenesis, by changing the level of expression or activity of an AAP.

6. Disease and disorders

[0247] Diseases and disorders that are characterized by increased AAP levels or biological activity may be treated with therapeutics that antagonize (i.e., reduce or inhibit) activity. Antagonists may be administered in a therapeutic or prophylactic manner. Therapeutics that may be used include: (1) AAP peptides, or analogs, derivatives, fragments or homologs thereof; (2) Abs to an AAP peptide; (3) AAP nucleic acids; (4) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (i.e., due to a heterologous insertion within the coding sequences) that are used to eliminate endogenous function of by homologous recombination (Capecchi, 1989); or (5) modulators (i.e., inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or Abs specific to an AAP) that alter the interaction between an AAP and its binding partner.

[0248] Diseases and disorders that are characterized by decreased AAP levels or biological activity may be treated with therapeutics that increase (i.e., are agonists to) activity. Therapeutics that upregulate activity may be administered therapeutically or prophylactically. Therapeutics that may be used include peptides, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

[0249] Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (e.g., from biopsy tissue) and assaying *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or AAP mRNAs). Methods include, but are not limited to, immunoassays (e.g., by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (e.g., Northern assays, dot blots, *in situ* hybridization, and the like).

7. Prophylactic methods

[0250] The invention provides but does not claim method for preventing, in a subject, a disease or condition associated with an aberrant AAP expression or activity, by administering an agent that modulates an AAP expression or at least one AAP activity. Subjects at risk for a disease that is caused or contributed to by an aberrant AAP expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the AAP aberrancy, such that a disease or

disorder is prevented or, alternatively, delayed in its progression Depending on the type of AAP aberrancy, for example, an AAP agonist or AAP antagonist can be used to treat the subject. The appropriate agent can be determined based on screening assays.

8. Therapeutic methods

[0251] Another aspect of the invention which is not claimed pertains to methods of modulating an AAP expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of AAP activity associated with the cell. An agent that modulates AAP activity can be a nucleic acid or a protein, a naturally occurring cognate ligand of an AAP, a peptide, an AAP peptidomimetic, or other small molecule. The agent may stimulate AAP activity. Examples of such stimulatory agents include an active AAP and an AAP nucleic acid molecule that has been introduced into the cell. In another embodiment, the agent inhibits AAP activity. Examples of inhibitory agents include antisense AAP nucleic acids and anti-AAP Abs. Modulatory methods can be performed *in vitro* (e.g., by culturing the cell with the agent) or, alternatively, *in vivo* (e.g., by administering the agent to a subject). As such, the invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of an AAP or nucleic acid molecule. In one embodiment, the method involves administering an agent (e.g., an agent identified by a screening assay), or combination of agents that modulates (e.g., up-regulates or down-regulates) AAP expression or activity. In another embodiment, the method involves administering an AAP or nucleic acid molecule as therapy to compensate for reduced or aberrant AAP expression or activity.

[0252] Stimulation of AAP activity is desirable in situations in which AAP is abnormally down-regulated and/or in which increased AAP activity is likely to have a beneficial effect. One example of such a situation is where a subject has a disorder characterized by aberrant angiogenesis (e.g., cancer).

9. Determination of the biological effect of the therapeutic

[0253] Suitable *in vitro* or *in vivo* assays can be performed to determine the effect of a specific therapeutic and whether its administration is indicated for treatment of the affected tissue.

[0254] In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given therapeutic exerts the desired effect upon the cell type(s). Modalities for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

10. Prophylactic and therapeutic uses, of the compositions of the invention

[0255] AAP nucleic acids and proteins are useful in potential prophylactic and therapeutic applications implicated in a variety of disorders including, but not limited to those related to angiogenesis.

[0256] As an example, a cDNA encoding an AAP may be useful in gene therapy, and the protein may be useful when administered to a subject in need thereof.

[0257] AAP nucleic acids, or fragments thereof, may also be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein is to be assessed. A further use could be as an anti-bacterial molecule (*i.e.*, some peptides have been found to possess anti-bacterial properties). These materials are further useful in the generation of Abs that immunospecifically bind to the novel substances of the invention for use in therapeutic or diagnostic methods.

[0258] The following example is meant to not be limiting.

EXAMPLE

Identification of genes differentially-regulated

[0259] A comprehensive mRNA profiling technique (GeneCalling) was used to determine differential gene expression profiles of human endothelial cells undergoing differentiation into tube-like structures (Kahn *et al.*, 2000). To confirm the expression data from GeneCalling, independent experiments were undertaken that used gene-specific PCR oligonucleotide primer pairs and an oligonucleotide probe labeled with a fluorescent dye at the 5' end and quencher fluorescent dye at the 3' end.. Total RNA (50 ng) was added to a 50 μ l RT-PCR mixture and run. The following data were collected:

hEF G	collagen gel 24 hr versus 4h	4.5 fold upregulated
hTRG	collagen gel 24 hr versus 4h	3.5 fold upregulated

(continued)

KLP	collagen gel 24 hr versus 4h	3.5 fold upregulated
myosin X	collagen gel 24 hr versus 4h	3.5 fold upregulated
NHR	collagen gel 24 hr versus 4h	7.3 fold downregulated
HBAZF	collagen gel 24 hr versus 4h	2.1 fold upregulated

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10 Tyr Thr Leu His Ala Ala Ile Pro Pro Leu Glu Glu Val Tyr Ser Leu
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Cys Glu Arg Leu Glu Lys Arg Arg Thr Ser Phe Leu Glu Gly Thr Leu
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Glu Gln Met Leu Asp Met Trp Ile Lys Glu Glu Val Ser Ser Ala Arg
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Gln Ala Met Ala Lys Tyr Met Ala Leu Ile Lys Glu Trp Pro Gly Tyr
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	Ile Lys Ile Phe Asn Ser Leu Gln Gln Leu Glu Ser Met Ser Asp Pro	
	1570	1575 1580
10	Ile Pro Ile Ile Gln Gly Ile Leu Gln Thr Gly His Asp Leu Arg Pro	
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	Leu Arg Asp Glu Leu Tyr Cys Gln Leu Ile Lys Gln Thr Asn Lys Val	
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15	Pro His Pro Gly Ser Val Gly Asn Leu Tyr Ser Trp Gln Ile Leu Thr	
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	Cys Leu Ser Cys Thr Phe Leu Pro Ser Arg Gly Ile Leu Lys Tyr Leu	
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	Lys Phe His Leu Lys Arg Ile Arg Glu Gln Phe Pro Gly Thr Glu Met	
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	Arg Glu Phe Val Pro Ser Arg Asp Glu Ile Glu Ala Leu Ile His Arg	
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	1745	1750 1755 1760
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	1765	1770 1775
	Gly Asp Leu Pro Trp Lys Phe Tyr Phe Lys Leu Tyr Cys Phe Leu Asp	
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	Thr Asp Asn Val Pro Lys Asp Ser Val Glu Phe Ala Phe Met Phe Glu	
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	1825	1830 1835 1840

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 1845 1850 1855
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Thr Lys Leu Leu Lys Ala Leu Lys Gly Tyr Ile Lys His Glu Ala Arg
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Lys Gly Asn Glu Asn Gln Asp Glu Ser Gln Thr Ser Ala Ser Ser Cys
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					245					250					255		
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	305					310					315					320	
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	Trp	Glu	Asp	Ile	Asp	Trp	Ile	Asp	Asn	Gly	Glu	Cys	Leu	Asp	Leu	Ile	
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30	Gly	Gln	Ile	Ala	Arg	Arg	Val	Tyr	Arg	Gln	Leu	Leu	Ala	Glu	Lys	Arg	
					805					810					815		
	Glu	Gln	Glu	Glu	Lys	Lys	Lys	Gln	Glu	Glu	Glu	Glu	Lys	Lys	Lys	Arg	
35					820				825					830			
	Glu	Glu	Glu	Glu	Arg	Glu	Arg	Glu	Arg	Glu	Arg	Arg	Glu	Ala	Glu	Leu	
			835					840					845				
40	Arg	Ala	Gln	Gln	Glu	Glu	Glu	Thr	Arg	Lys	Gln	Gln	Glu	Leu	Glu	Ala	
		850					855						860				
	Leu	Gln	Lys	Ser	Gln	Lys	Glu	Ala	Glu	Leu	Thr	Arg	Glu	Leu	Glu	Lys	
	865					870					875					880	
45	Gln	Lys	Glu	Asn	Lys	Gln	Val	Glu	Glu	Ile	Leu	Arg	Leu	Glu	Lys	Glu	
					885					890					895		
	Ile	Glu	Asp	Leu	Gln	Arg	Met	Lys	Glu	Gln	Gln	Glu	Leu	Ser	Leu	Thr	
				900					905					910			
50	Glu	Ala	Ser	Leu	Gln	Lys	Leu	Gln	Glu	Arg	Arg	Asp	Gln	Glu	Leu	Arg	
			915					920					925				
	Arg	Leu	Glu	Glu	Glu	Ala	Cys	Arg	Ala	Ala	Gln	Glu	Phe	Leu	Glu	Ser	
55							930					940					

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	Leu Asn Phe Asp Glu Ile Asp Glu Cys Val Arg Asn Ile Glu Arg Ser	
	945	950 955 960
5	Leu Ser Val Gly Ser Glu Phe Ser Ser Glu Leu Ala Glu Ser Ala Cys	
		965 970 975
	Glu Glu Lys Pro Asn Phe Asn Phe Ser Gln Pro Tyr Pro Glu Glu Glu	
		980 985 990
10	Val Asp Glu Gly Phe Glu Ala Asp Asp Asp Ala Phe Lys Asp Ser Pro	
		995 1000 1005
	Asn Pro Ser Glu His Gly His Ser Asp Gln Arg Thr Ser Gly Ile Arg	
		1010 1015 1020
15	Thr Ser Asp Asp Ser Ser Glu Glu Asp Pro Tyr Met Asn Asp Thr Val	
		1025 1030 1035 1040
	Val Pro Thr Ser Pro Ser Ala Asp Ser Thr Val Leu Leu Ala Pro Ser	
20		1045 1050 1055
	Val Gln Asp Ser Gly Ser Leu His Asn Ser Ser Ser Gly Glu Ser Thr	
		1060 1065 1070
25	Tyr Cys Met Pro Gln Asn Ala Gly Asp Leu Pro Ser Pro Asp Gly Asp	
		1075 1080 1085
	Tyr Asp Tyr Asp Gln Asp Asp Tyr Glu Asp Gly Ala Ile Thr Ser Gly	
		1090 1095 1100
30	Ser Ser Val Thr Phe Ser Asn Ser Tyr Gly Ser Gln Trp Ser Pro Asp	
		1105 1110 1115 1120
	Tyr Arg Cys Ser Val Gly Thr Tyr Asn Ser Ser Gly Ala Tyr Arg Phe	
		1125 1130 1135
35	Ser Ser Glu Gly Ala Gln Ser Ser Phe Glu Asp Ser Glu Glu Asp Phe	
		1140 1145 1150
	Asp Ser Arg Phe Asp Thr Asp Asp Glu Leu Ser Tyr Arg Arg Asp Ser	
		1155 1160 1165
40	Val Tyr Ser Cys Val Thr Leu Pro Tyr Phe His Ser Phe Leu Tyr Met	
		1170 1175 1180
	Lys Gly Gly Leu Met Asn Ser Trp Lys Arg Arg Trp Cys Val Leu Lys	
45		1185 1190 1195 1200
	Asp Glu Thr Phe Leu Trp Phe Arg Ser Lys Gln Glu Ala Leu Lys Gln	
		1205 1210 1215
50	Gly Trp Leu His Lys Lys Gly Gly Gly Ser Ser Thr Leu Ser Arg Arg	
		1220 1225 1230
	Asn Trp Lys Lys Arg Trp Phe Val Leu Arg Gln Ser Lys Leu Met Tyr	
		1235 1240 1245
55		

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Phe Glu Asn Asp Ser Glu Glu Lys Leu Lys Gly Thr Val Glu Val Arg
 1250 1255 1260
 5 Thr Ala Lys Glu Ile Ile Asp Asn Thr Thr Lys Glu Asn Gly Ile Asp
 1265 1270 1275 1280
 Ile Ile Met Ala Asp Arg Thr Phe His Leu Ile Ala Glu Ser Pro Glu
 1285 1290 1295
 10 Asp Ala Ser Gln Trp Phe Ser Val Leu Ser Gln Val His Ala Ser Thr
 1300 1305 1310
 Asp Gln Glu Ile Gln Glu Met His Asp Glu Gln Ala Asn Pro Gln Asn
 1315 1320 1325
 15 Ala Val Gly Thr Leu Asp Val Gly Leu Ile Asp Ser Val Cys Ala Ser
 1330 1335 1340
 Asp Ser Pro Asp Arg Pro Asn Ser Phe Val Ile Ile Thr Ala Asn Arg
 1345 1350 1355 1360
 20 Val Leu His Cys Asn Ala Asp Thr Pro Glu Glu Met His His Trp Ile
 1365 1370 1375
 Thr Leu Leu Gln Arg Ser Lys Gly Asp Thr Arg Val Glu Gly Gln Glu
 1380 1385 1390
 Phe Ile Val Arg Gly Trp Leu His Lys Glu Val Lys Asn Ser Pro Lys
 1395 1400 1405
 30 Met Ser Ser Leu Lys Leu Lys Lys Arg Trp Phe Val Leu Thr His Asn
 1410 1415 1420
 Ser Leu Asp Tyr Tyr Lys Ser Ser Glu Lys Asn Ala Leu Lys Leu Gly
 1425 1430 1435 1440
 35 Thr Leu Val Leu Asn Ser Leu Cys Ser Val Val Pro Pro Asp Glu Lys
 1445 1450 1455
 Ile Phe Lys Glu Thr Gly Tyr Trp Asn Val Thr Val Tyr Gly Arg Lys
 1460 1465 1470
 40 His Cys Tyr Arg Leu Tyr Thr Lys Leu Leu Asn Glu Ala Thr Arg Trp
 1475 1480 1485
 Ser Ser Ala Ile Gln Asn Val Thr Asp Thr Lys Ala Pro Ile Asp Thr
 1490 1495 1500
 Pro Thr Gln Gln Leu Ile Gln Asp Ile Lys Glu Asn Cys Leu Asn Ser
 1505 1510 1515 1520
 50 Asp Val Val Glu Gln Ile Tyr Lys Arg Asn Pro Ile Leu Arg Tyr Thr
 1525 1530 1535
 His His Pro Leu His Ser Pro Leu Leu Pro Leu Pro Tyr Gly Asp Ile
 1540 1545 1550

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	Asn	Leu	Asn	Leu	Leu	Lys	Asp	Lys	Gly	Tyr	Thr	Thr	Leu	Gln	Asp	Glu	
5	Ala	Ile	Lys	Ile	Phe	Asn	Ser	Leu	Gln	Gln	Leu	Glu	Ser	Met	Ser	Asp	
	Pro	Ile	Pro	Ile	Ile	Gln	Gly	Ile	Leu	Gln	Thr	Gly	His	Asp	Leu	Arg	
10	Pro	Leu	Arg	Asp	Glu	Leu	Tyr	Cys	Gln	Leu	Ile	Lys	Gln	Thr	Asn	Lys	
	Val	Pro	His	Pro	Gly	Ser	Val	Gly	Asn	Leu	Tyr	Ser	Trp	Gln	Ile	Leu	
15	Thr	Cys	Leu	Ser	Cys	Thr	Phe	Leu	Pro	Ser	Arg	Gly	Ile	Leu	Lys	Tyr	
20	Leu	Lys	Phe	His	Leu	Lys	Arg	Ile	Arg	Glu	Gln	Phe	Pro	Gly	Thr	Glu	
	Met	Glu	Lys	Tyr	Ala	Leu	Phe	Thr	Tyr	Glu	Ser	Leu	Lys	Lys	Thr	Lys	
25	Cys	Arg	Glu	Phe	Val	Pro	Ser	Arg	Asp	Glu	Ile	Glu	Ala	Leu	Ile	His	
	Arg	Gln	Glu	Met	Thr	Ser	Thr	Val	Tyr	Cys	His	Gly	Gly	Gly	Ser	Cys	
30	Lys	Ile	Thr	Ile	Asn	Ser	His	Thr	Thr	Ala	Gly	Glu	Val	Val	Glu	Lys	
	Leu	Ile	Arg	Gly	Leu	Ala	Met	Glu	Asp	Ser	Arg	Asn	Met	Phe	Ala	Leu	
35	Phe	Glu	Tyr	Asn	Gly	His	Val	Asp	Lys	Ala	Ile	Glu	Ser	Arg	Thr	Val	
	Val	Ala	Asp	Val	Leu	Ala	Lys	Phe	Glu	Lys	Leu	Ala	Ala	Thr	Ser	Glu	
40	Val	Gly	Asp	Leu	Pro	Trp	Lys	Phe	Tyr	Phe	Lys	Leu	Tyr	Cys	Phe	Leu	
	Asp	Thr	Asp	Asn	Val	Pro	Lys	Asp	Ser	Val	Glu	Phe	Ala	Phe	Met	Phe	
45	Glu	Gln	Ala	His	Glu	Ala	Val	Ile	His	Gly	His	His	Pro	Ala	Pro	Glu	
	Glu	Asn	Leu	Gln	Val	Leu	Ala	Ala	Leu	Arg	Leu	Gln	Tyr	Leu	Gln	Gly	
50	Asp	Tyr	Thr	Leu	His	Ala	Ala	Ile	Pro	Pro	Leu	Glu	Glu	Val	Tyr	Ser	

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Leu Gln Arg Leu Lys Ala Arg Ile Ser Gln Ser Thr Lys Thr Phe Thr
 1860 1865 1870
 5 Pro Cys Glu Arg Leu Glu Lys Arg Arg Thr Ser Phe Leu Glu Gly Thr
 1875 1880 1885
 Leu Arg Arg Ser Phe Arg Thr Gly Ser Val Val Arg Gln Lys Val Glu
 1890 1895 1900
 10 Glu Glu Gln Met Leu Asp Met Trp Ile Lys Glu Glu Val Ser Ser Ala
 1905 1910 1915 1920
 Arg Ala Ser Ile Ile Asp Lys Trp Arg Lys Phe Gln Gly Met Asn Gln
 15 1925 1930 1935
 Glu Gln Ala Met Ala Lys Tyr Met Ala Leu Ile Lys Glu Trp Pro Gly
 1940 1945 1950
 20 Tyr Gly Ser Thr Leu Phe Asp Val Glu Cys Lys Glu Gly Gly Phe Pro
 1955 1960 1965
 Gln Glu Leu Trp Leu Gly Val Ser Ala Asp Ala Val Ser Val Tyr Lys
 1970 1975 1980
 25 Arg Gly Glu Gly Arg Pro Leu Glu Val Phe Gln Tyr Glu His Ile Leu
 1985 1990 1995 2000
 Ser Phe Gly Ala Pro Leu Ala Asn Thr Tyr Lys Ile Val Val Asp Glu
 2005 2010 2015
 30 Arg Glu Leu Leu Phe Glu Thr Ser Glu Val Val Asp Val Ala Lys Leu
 2020 2025 2030
 Met Lys Ala Tyr Ile Ser Met Ile Val Lys Lys Arg Tyr Ser Thr Thr
 35 2035 2040 2045
 Arg Ser Ala Ser Ser Gln Gly Ser Ser Arg
 2050 2055
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Claims

- 45 1. An isolated polypeptide comprising an amino acid sequence having at least 90% sequence identity to the sequence of SEQ ID NO: 4, wherein expression of the polypeptide is upregulated during angiogenesis.
2. A polypeptide according to Claim 1 wherein said amino acid sequence comprises SEQ ID NO: 4.
- 50 3. A polypeptide according to Claim 1, wherein said amino acid sequence has at least 95% sequence identity to the sequence of SEQ ID NO: 4.
4. An isolated polynucleotide encoding the polypeptide of any of Claims 1-3, or a complement of said polynucleotide.
- 55 5. An isolated polynucleotide comprising a nucleotide sequence having at least 80% sequence identity to the sequence of SEQ ID NO: 3, or a complement of said polynucleotide, wherein expression of the polynucleotide is upregulated during angiogenesis.

6. A polynucleotide according to Claim 5, wherein said nucleotide sequence has at least 90% sequence identity to the sequence of SEQ ID NO: 3, or a complement of said polynucleotide.
- 5 7. A polynucleotide according to Claim 5, wherein said nucleotide sequence has at least 98% sequence identity to the sequence of SEQ ID NO: 3, or a complement of said polynucleotide.
8. A vector comprising a polynucleotide according to any of Claims 4-7.
9. A cell comprising a vector according to Claim 8.
- 10 10. An antibody that specifically binds to a polypeptide according to any of Claims 1-3.
11. A method of detecting angiogenesis in a tissue sample, comprising measuring expression of a polypeptide according to any of Claims 1-3 or a polynucleotide according to any of Claims 4-7 in the tissue sample.
- 15 12. A method according to Claim 11, wherein detecting angiogenesis indicates the presence of cancer or tumour.
13. A method of identifying an antagonist of angiogenesis, comprising;
20 a) contacting a cell or tissue sample undergoing angiogenesis with a candidate agent; and
 b) detecting expression of a polypeptide according to any of Claims 1-3 or a polynucleotide according to any of Claims 4-7, wherein a candidate compound that decreases expression of the polypeptide is identified as an antagonist of angiogenesis.
- 25 14. A method of identifying an agonist of angiogenesis, comprising:
 a) contacting a cell or tissue sample undergoing angiogenesis with a candidate compound; and
 b) detecting expression of a polypeptide according to any of Claims 1-3 or a polynucleotide according to any of Claims 4-7, wherein a candidate compound that increases expression of the polypeptide is identified as an
30 agonist of angiogenesis.
15. A method of screening a tissue sample for tumorigenic potential, comprising: measuring expression of a polypeptide according to any one of Claims 1-3 or a polynucleotide according to any one of Claims 4-7 in said tissue sample.
- 35 16. A method of determining the clinical stage of a tumour in a subject comprising:
 a) detecting expression of a polypeptide according to any of Claims 1-3 or a polynucleotide according to any of Claims 4-7 in a tissue sample from the subject; and
 b) comparing expression of the polypeptide to expression of the polypeptide in a control sample.
- 40 17. A method of monitoring the effectiveness of a treatment for an angiogenic disorder in a subject, comprising detecting expression of a polypeptide according to any of Claims 1-3 in a tissue sample from the subject, wherein a decrease in expression of the polypeptide indicates efficacy of treatment.
- 45 18. A method according to Claim 17, wherein the angiogenic disorder is cancer or tumor.
19. An *in vitro* method for determining whether a compound up-regulates or down-regulates expression of a polynucleotide according to any of Claims 4-7, comprising contacting a cell or tissue with the compound and detecting expression of the polynucleotide.
- 50 20. A transgenic non-human animal, having a disruption in a polynucleotide having at least 80% sequence identity to SEQ ID NO: 3, wherein the disruption prevents expression of a polypeptide encoded by the sequence.
21. A transgenic non-human animal according to Claim 20, wherein the non-human animal is a mouse.
- 55 22. A transgenic non-human animal, comprising an exogenous polynucleotide having at least 80% sequence identity to the sequence of SEQ ID NO: 3, or a complement of said polynucleotide.

23. A transgenic non-human animal according to Claim 22, wherein said exogenous polynucleotide has at least 90% sequence identity to the sequence of SEQ ID NO: 3, or a complement of said polynucleotide, preferably at least 98% sequence identity to the sequence of SEQ ID NO: 3, or a complement of said polynucleotide.

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Patentansprüche

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1. Isoliertes Polypeptid, umfassend eine Aminosäuresequenz, die mindestens 90% Sequenzidentität mit der Sequenz mit SEQ ID Nr.: 4 aufweist, wobei die Expression des Polypeptids während der Angiogenese nach oben reguliert wird.

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2. Polypeptid nach Anspruch 1, wobei die Aminosäuresequenz SEQ ID Nr.: 4 umfasst.

3. Polypeptid nach Anspruch 1, wobei die Aminosäuresequenz mindestens 95% Sequenzidentität mit der Sequenz mit SEQ ID Nr.: 4 aufweist.

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4. Isoliertes Polynukleotid, kodierend für das Polypeptid nach einem der Ansprüche 1-3, oder ein Komplement des Polynukleotids.

5. Isoliertes Polynukleotid, umfassend eine Nukleotidsequenz, die mindestens 80% Sequenzidentität mit der Sequenz mit SEQ ID Nr.: 3 aufweist, oder ein Komplement des Polynukleotids, wobei die Expression des Polynukleotids während der Angiogenese nach oben reguliert wird.

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6. Polynukleotid nach Anspruch 5, wobei die Nukleotidsequenz mindestens 90% Sequenzidentität mit der Sequenz mit SEQ ID Nr.: 3 aufweist, oder ein Komplement des Polynukleotids.

7. Polynukleotid nach Anspruch 5, wobei die Nukleotidsequenz mindestens 98% Sequenzidentität mit der Sequenz mit SEQ ID Nr.: 3 aufweist, oder ein Komplement des Polynukleotids.

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8. Vektor, umfassend ein Polynukleotid nach einem der Ansprüche 4-7.

9. Zelle, umfassend einen Vektor nach Anspruch 8.

10. Antikörper, der spezifisch an ein Polypeptid nach einem der Ansprüche 1-3 bindet.

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11. Verfahren zum Nachweisen von Angiogenese in einer Gewebeprobe, umfassend das Messen der Expression eines Polypeptids nach einem der Ansprüche 1-3 oder eines Polynukleotids nach einem der Ansprüche 4-7 in der Gewebeprobe.

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12. Verfahren nach Anspruch 11, wobei das Nachweisen einer Angiogenese das Vorhandensein von Krebs oder eines Tumors anzeigt.

13. Verfahren zum Identifizieren eines Angiogeneseantagonisten, umfassend:

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- a) In-Kontakt-Bringen einer Zell- oder Gewebeprobe, welche Angiogenese erfährt, mit einem Kandidatenagens; und
- b) Nachweisen der Expression eines Polypeptids nach einem der Ansprüche 1-3 oder eines Polynukleotids nach einem der Ansprüche 4-7, wobei eine Kandidatenverbindung, welche die Expression des Polypeptids verringert, als Angiogeneseantagonist identifiziert wird.

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14. Verfahren zum Identifizieren eines Angiogeneseagonisten, umfassend:

- a) In-Kontakt-Bringen einer Zell- oder Gewebeprobe mit einer Kandidatenverbindung; und
- b) Nachweisen der Expression eines Polypeptids nach einem der Ansprüche 1-3 oder eines Polynukleotids nach einem der Ansprüche 4-7, wobei eine Kandidatenverbindung, welche die Expression des Polypeptids steigert, als Angiogeneseagonist identifiziert wird.

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15. Verfahren zum Durchsuchen einer Gewebeprobe auf tumorigenes Potential, umfassend:

Messen der Expression eines Polypeptids nach einem der Ansprüche 1-3 oder eines Polynukleotids nach einem der Ansprüche 4-7 in der Gewebeprobe.

16. Verfahren zum Bestimmen des klinischen Stadiums eines Tumors in einem Probanden, umfassend:

- a) Nachweisen der Expression eines Polypeptids nach einem der Ansprüche 1-3 oder eines Polynukleotids nach einem der Ansprüche 4-7 in einer Gewebeprobe aus dem Probanden; und
- b) Vergleichen der Expression des Polypeptids mit der Expression des Polypeptids in einer Kontrollprobe.

17. Verfahren zum Überwachen der Wirksamkeit einer Behandlung für eine angiogene Funktionsstörung in einem Probanden, umfassend das Nachweisen der Expression eines Polypeptids nach einem der Ansprüche 1-3 in einer Gewebeprobe aus dem Probanden, wobei eine Abnahme der Expression des Polypeptids die Effizienz der Behandlung anzeigt.

18. Verfahren nach Anspruch 14, wobei die angiogene Funktionsstörung Krebs oder ein Tumor ist.

19. *In vitro* Verfahren zum Bestimmen, ob eine Verbindung die Expression eines Polynukleotids nach einem der Ansprüche 4-7 nach oben reguliert oder nach unten reguliert, umfassend das In-Kontakt-Bringen einer Zelle oder eines Gewebes mit der Verbindung und das Nachweisen der Expression des Polynukleotids.

20. Transgenes nichtmenschliches Lebewesen, das eine Disruption hat in einem Polynukleotid, das mindestens 80% Sequenzidentität mit SEQ ID Nr.: 3 aufweist, wobei die Disruption der Expression eines Polypeptids vorbeugt, für das von der Sequenz kodiert wird.

21. Transgenes nichtmenschliches Lebewesen nach Anspruch 20, wobei das nichtmenschliche Lebewesen eine Maus ist.

22. Transgenes nichtmenschliches Lebewesen, umfassend ein exogenes Polynukleotid, das mindestens 80% Sequenzidentität mit der Sequenz mit SEQ ID Nr.: 3 aufweist, oder ein Komplement des Polynukleotids.

23. Transgenes nichtmenschliches Lebewesen nach Anspruch 22, wobei das exogene Polynukleotid mindestens 90% Sequenzidentität mit der Sequenz mit SEQ ID Nr.: 3 aufweist, oder ein Komplement des Polynukleotids, und vorzugsweise mindestens 98% Sequenzidentität mit der Sequenz mit SEQ ID Nr.: 3 aufweist, oder ein Komplement des Polynukleotids.

Revendications

1. Polypeptide isolé comprenant une séquence d'acides aminés ayant une identité de séquence d'au moins 90 % avec la séquence SEQ ID NO: 4, où l'expression du polypeptide est régulée à la hausse au cours de l'angiogenèse.

2. Polypeptide selon la revendication 1, où ladite séquence d'acides aminés comprend la SEQ ID NO:4.

3. Polypeptide selon la revendication 1, où ladite séquence d'acides aminés a une identité de séquence d'au moins 95 % avec la séquence SEQ ID NO:4.

4. Polynucléotide isolé codant le polypeptide selon l'une quelconque des revendications 1 à 3, ou complément dudit polynucléotide.

5. Polynucléotide isolé comprenant une séquence de nucléotide ayant une identité de séquence d'au moins 80 % avec la séquence SEQ ID NO: 3, ou complément dudit polynucléotide, où l'expression du polynucléotide est régulée à la hausse au cours de l'angiogenèse.

6. Polynucléotide selon la revendication 5, où ladite séquence de nucléotide a une identité de séquence d'au moins 90 % avec la séquence SEQ ID NO: 3, ou un complément dudit polynucléotide.

7. Polynucléotide selon la revendication 5, où ladite séquence de nucléotide a une identité de séquence d'au moins 98 % avec la séquence SEQ ID NO: 3, ou un complément dudit polynucléotide.

8. Vecteur comprenant un polynucléotide selon l'une quelconque des revendications 4 à 7.
9. Cellule comprenant un vecteur selon la revendication 8.
- 5 10. Anticorps qui lie spécifiquement un polypeptide selon l'une quelconque des revendications 1 à 3.
11. Procédé de détection de l'angiogenèse dans un échantillon de tissu, comprenant la mesure de l'expression d'un polypeptide selon l'une quelconque des revendications 1 à 3 ou d'un polynucléotide selon l'une quelconque des revendications 4 à 7 dans l'échantillon de tissu.
- 10 12. Procédé selon la revendication 11, dans lequel la détection de l'angiogenèse indique la présence d'un cancer ou d'une tumeur.
13. Procédé d'identification d'un antagoniste de l'angiogenèse, comprenant :
15 a) la mise en contact d'une cellule ou d'un échantillon de tissu subissant l'angiogenèse avec un agent candidat ; et
 b) la détection de l'expression d'un polypeptide selon l'une quelconque des revendications 1 à 3 ou d'un polynucléotide selon l'une quelconque des revendications 4 à 7, où un composé candidat qui diminue l'expression du polypeptide est identifié comme antagoniste de l'angiogenèse.
- 20 14. Procédé d'identification d'un agoniste de l'angiogenèse, comprenant :
 a) la mise en contact d'une cellule ou d'un échantillon de tissu avec un composé candidat ; et
 b) la détection de l'expression d'un polypeptide selon l'une quelconque des revendications 1 à 3 ou d'un polynucléotide selon l'une quelconque des revendications 4 à 7, où un composé candidat qui augmente l'expression du polypeptide est identifié comme agoniste de l'angiogenèse.
- 25 15. Procédé de criblage d'un échantillon de tissu pour le potentiel tumorigène, comprenant : la mesure de l'expression d'un polypeptide selon l'une quelconque des revendications 1 à 3 ou d'un polynucléotide selon l'une quelconque des revendications 4 à 7 dans ledit échantillon de tissu.
- 30 16. Procédé de détermination du stade clinique d'une tumeur chez un sujet, comprenant :
 a) la détection de l'expression d'un polypeptide selon l'une quelconque des revendications 1 à 3 ou d'un polynucléotide selon l'une quelconque des revendications 4 à 7 dans un échantillon de tissu prélevé chez un sujet ; et
 b) la comparaison de l'expression du polypeptide à l'expression du polypeptide dans un échantillon témoin.
- 35 17. Procédé de surveillance de l'efficacité d'un traitement pour un trouble angiogénique chez un sujet, comprenant la détection de l'expression d'un polypeptide selon l'une quelconque des revendications 1 à 3 dans un échantillon de tissu prélevé chez le sujet, où une diminution de l'expression du polypeptide indique l'efficacité du traitement.
- 40 18. Procédé selon la revendication 14, où le trouble angiogénique est le cancer ou la tumeur.
19. Procédé *in vitro* permettant de déterminer si un composé régule à la hausse ou à la baisse l'expression d'un polynucléotide selon l'une quelconque des revendications 4 à 7, comprenant la mise en contact d'une cellule ou d'un tissu avec le composé et la détection de l'expression du polynucléotide.
- 45 20. Animal non humain transgénique, ayant une perturbation dans un polynucléotide, ayant une identité de séquence d'au moins 80 % avec la SEQ ID NO: 3, où la perturbation empêche l'expression d'un polypeptide codé par la séquence.
- 50 21. Animal non humain transgénique selon la revendication 20, où l'animal non humain est une souris.
22. Animal non humain transgénique, comprenant un polynucléotide exogène ayant une identité de séquence d'au moins 80 % avec la SEQ ID NO: 3, ou un complément dudit polynucléotide.
- 55 23. Animal non humain transgénique selon la revendication 22, où ledit polynucléotide exogène a une identité de séquence d'au moins 90 % avec la séquence SEQ ID NO: 3, ou complément dudit polynucléotide, de préférence

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une identité de séquence d'au moins 98 % avec la séquence de SEQ ID NO: 3, ou un complément dudit polynucleotide.

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